

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: December 12, 2003, 14:43:27 ; Search time 52.1387 Seconds  
(without alignments)  
2036.647 Million cell updates/sec

Title: PCT-US03-24332-6

Perfect score: 3343  
Sequence: 1 KDYKDDDLAAANXALRGT.....GDTSGDYKALLLCGGEDD 669

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_194un03.\*  
1: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.\*  
2: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*  
3: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*  
4: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.\*  
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23: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*  
24: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	3337	99.8	669	24 ABP56249
2	1708	51.1	786	11 AAR03726
3	1706	51.0	672	11 AAR03725
4	1688	50.5	675	24 AB054621
5	1593	47.7	319	24 ABP56248
6	1580	47.3	318	20 AA113925
7	1570	47.0	319	16 AAR75695
8	1558	46.6	736	22 AAB19948
9	1530	45.8	319	20 AA113924

10	1530	45.8	319	23 AAB57067
11	1452.5	43.4	600	21 AAY92930
12	1451.5	43.4	319	13 AAR26276
13	1451.5	43.4	319	14 AAR41021
14	1451.5	43.4	319	23 ABB32550
15	1451.5	43.4	320	9 AAB80511
16	1451.5	43.4	320	10 AAB1953
17	1451.5	43.4	320	12 AAR13082
18	1451.5	43.4	320	20 AAY13923
19	1451.5	43.4	320	21 AAB4788
20	1451.5	43.4	320	23 AAG31220
21	1448.5	43.3	320	10 AAB20053
22	1447.5	43.3	320	9 AAB2317
23	1447.5	43.3	320	13 AAR26180
24	1445.5	43.2	320	9 AAB80242
25	1445.5	43.2	320	9 AAB80714
26	1445.5	43.2	320	12 AAR11910
27	1442.5	43.1	327	22 AAB50863
28	1442.5	43.1	327	22 AAB50864
29	1442.5	43.1	327	22 AAB50865
30	1441.5	43.1	320	10 AAB1363
31	1419.5	42.5	319	13 AAR25718
32	921	27.6	321	20 AAY13926
33	921	27.6	321	23 AAB56279
34	921	27.6	324	23 AAB43617
35	920	27.5	321	10 AAB1913
36	904.5	27.1	320	21 AAY84790
37	887	26.5	208	21 AAB58353
38	871	26.1	503	14 AAR34127
39	863	25.8	503	14 AAR34128
40	860	25.7	505	20 AAY07117
41	852	25.5	299	23 AAB56354
42	822.5	24.6	327	9 AAB80715
43	822.5	24.6	327	10 AAB1954
44	822.5	24.6	327	14 AAR35754
45	822.5	24.6	327	22 AAB78655

## ALIGNMENTS

RESULT 1	ABP56249	standard; Protein: 669 AA.
ID	ABP56249	
XX	AC	ABP56249;
XX	DT	28-MAR-2003 (first entry)
XX	DE	Modified annexin protein SEQ ID NO:6.
KW	Annexin, modified; thrombosis; annexin V; thrombolytic;	
KW	coronary thrombosis; overt cerebral thrombosis; arterial	
KW	transient cerebral ischaemic attack; venous thrombosis.	
XX	OS	Homo sapiens.
OS	Synthetic.	
XX	XX	
PH	Key	Location/Qualifiers
FT	Misc-difference 15	/label= unknown
FT	Misc-difference 334	/note= "encoded by TCN"
FT	Misc-difference 334	/label= unknown
FT	Misc-difference 351	/note= "encoded by NNN"
FT	Misc-difference 351	/label= unknown
XX	FT	/note= "encoded by NNN"
XX	FT	/note= "encoded by NNN"
XX	XX	MO200267857-AA2.
XX	XX	06-SEP-2002.
XX	XX	

Mouse ischaemic co  
Annexin V/urolinase  
CPB-1. Homo sapie  
Calphobindin I (CP  
Human CPB-1 protei  
Placental coagul  
Vascular anti-coag  
PAP-1. Homo sapie  
5657 GFP variant/h  
Amino acid sequenc  
Human annexin V,  
anticoagulant p4  
PAP-1 isolated fro  
CPB-1. Homo sapie  
Sequence vascular  
Sequence vascular  
Vascular anticoagu  
Modified human ann  
Modified human ann  
Human lipocortin-V  
CPB-1. Homo sapie  
5657 GFP variant/h  
Human ovarian canc  
Human cancer associ  
Anticoagulative PP  
Amino acid sequenc  
Lung cancer associ  
Annexin XI type I  
Lung cancer associ  
Human polypeptide  
Sequence vascular  
Vascular anti-coag  
VAC-beta. Synthet  
Human protein SEQ

Pf		21.-FEB-2002; 2002MO-US05079.	
Xx			
Pr		21-FEB-2001; 2001US-270402P.	
Fr		21-NOV-2001; 2001US-332582P.	
Xx			
Xx		(SUUR-) SURROMED INC.	
Pa			
Xx		Allison A;	
Pi			
Dd		WPI; 2003-129062/12.	
Dr		N-PBDB; ABZ21926.	
Xx			
Pt		Novel isolated modified annexin proteins comprising annexin protein	
Pt		coupled to polyethylene glycol or additional proteins, useful for	
Pt		treating thrombosis e.g. coronary thrombosis and overt cerebral	
Pt		thrombosis -	
Xx			
Pt		Claim 6; Page 59-62; 62pp; English.	
Pt			
Cc		The present invention describes a modified annexin protein (I) comprising	
Cc		an annexin protein coupled to: (1) polyethylene glycol (PEG); or (1i) an	
Cc		additional protein. (I) has thrombolytic activity and can be used as a	
Cc		thrombolysis modulator, and an inhibitor of cellular and humoral	
Cc		mechanisms by which platelet aggregation is amplified. (I) can be used	
Cc		for treating a subject at risk from thrombosis. Preferably, a	
Cc		pharmaceutical composition comprising (I) is administered to a subject	
Cc		after coronary thrombosis, overt cerebral thrombosis, or transient	
Cc		cerebral ischemic attack. More preferably, the pharmaceutical	
Cc		composition is administered to a diabetic patient who is at risk of	
Cc		arterial thrombosis. The pharmaceutical composition can also be	
Cc		administered during pregnancy or parturition. (I) is also useful for	
Cc		treating arterial or venous thrombosis caused by any medical procedure	
Cc		or condition as described above. (I) prevents arterial or venous	
Cc		thrombosis without increasing haemorrhage. The present sequence	
Cc		represents a modified annexin protein from the present invention.	
Sq			
Xx		Sequence 669 AA;	
Qn		Query Match 99.8%; Score 3317; DB 24; Length 669;	
Bst		Best Local Similarity 100.0%; Pred. No. 8.9e-241;	
Mch		Matches 669; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
Oy			
Dd		1 MDYDDDDDKLAANXALRGTVYDPSGFDRAAEVLRRKAMGLGTDESDINLITARSNA 60	
Oy		1 MDYDDDDDKLAANXALRGTVYDPSGFDRAAEVLRRKAMGLGTDESDINLITARSNA 60	
Dd		61 QROQIAEEFFTLFGRLDVNDMKSSELTGFKEKILVALMKPSRLDYAYELKKAIGAGTDEX 120	
Oy		61 QROQIAEEFFTLFGRLDVNDMKSSELTGFKEKILVALMKPSRLDYAYELKKAIGAGTDEX 120	
Dd		121 VLETTISRPEELRAIKOAYEESYNSLEDVDVDTSGYQRMLVLLQANRPDPAID 180	
Oy		121 VLETTISRPEELRAIKOAYEESYNSLEDVDVDTSGYQRMLVLLQANRPDPAID 180	
Dd		121 VLETTISRPEELRAIKOAYEESYNSLEDVDVDTSGYQRMLVLLQANRPDPAID 180	
Oy		181 DAQVELDAOLFOAGELKMGTDSEKITITLGRSVSHLRVFYDKMTISGFOJETIDRE 240	
Dd		181 DAQVELDAOLFOAGELKMGTDSEKITITLGRSVSHLRVFYDKMTISGFOJETIDRE 240	
Oy		241 TSGNLEULLAAVVKRSRSTPAYLAETLYAMGAGATDHTLTRIVASSETDENIKER 3000	
Dd		241 TSGNLEULLAAVVKRSRSTPAYLAETLYAMGAGATDHTLTRIVASSETDENIKER 3000	
Oy		301 RKNFATSLSYMIKGDTSGDYKKALLLCGGEDDXSRSGLEVLFQGPSTYALRGTYDF 3600	
Dd		301 RKNFATSLSYMIKGDTSGDYKKALLLCGGEDDXSRSGLEVLFQGPSTYALRGTYDF 3600	
Oy		361 SGFGGRADAEVLKRKAKGCTGBDSITLNLTRSNANOQOIAEEFKTLFGDLVNDMKSE 4200	
Dd		361 SGFGGRADAEVLKRKAKGCTGBDSITLNLTRSNANOQOIAEEFKTLFGDLVNDMKSE 4200	
Oy		421 LTGFEKLIALVMKPSSLDYAVELKAKLAGAETDERVLTETIASRTPEELRAIKOAYEE 4800	
Dd		421 LTGFEKLIALVMKPSSLDYAVELKAKLAGAETDERVLTETIASRTPEELRAIKOAYEE 4800	

Qy	48	YGSNLEDDVDPGDSGYGMLVVLQANRDPPTALDPAQVLDPAQALFQAGELKMGTDDE	540
Db	481	YGSNLEDDVDPGDSGYGMLVVLQANRDPPTALDPAQVLDPAQALFQAGELKMGTDDE	540
Qy	541	KFTITIGTSVSHLRVRPDKYMTISGFOIEETIDRETSNGNIENLLAVKYSISIPAYLA	6000
Db	541	KFTITIGTSVSHLRVRPDKYMTISGFOIEETIDRETSNGNIENLLAVKYSISIPAYLA	6000
Qy	601	ETIYYAMKAGNDPHILRVIVSRSEIDLFTNRKSPFNKPAFTLSYMIKGPDSGDYKCAL	6600
Db	601	ETIYYAMKAGNDPHILRVIVSRSEIDLFTNRKSPFNKPAFTLSYMIKGPDSGDYKCAL	6600
Qy	661	LLLCGGEDD 669	
Db	661	LLLCGGEDD 669	

RESULT 2

AA03726	AA03726	standard; protein; 786 AA.
XX	AA03726;	
XX	AC	AA03726;
XX	DT	25-MAR-2003 (updated)
XX	DT	04-JUL-1990 (first entry)
XX	DE	Human placenta-derived coagulation inhibitor protein.
XX	DE	Human placenta-derived coagulation inhibitor; anticoagulant.
XX	KW	Human; placenta; coagulation inhibitor; anticoagulant.
XX	XX	
XX	OS	Homo sapiens.
XX	EN	EP51826-A.
XX	PD	24-JAN-1990.
XX	PF	19-JUL-1989; 89EP-0113261.
XX	PR	21-JUL-1988; 88JP-0182633.
XX	PA	(KOMA ) KOMA CO LTD.
XX	PI	Iwasaki A, Suda M, Saino Y;
XX	DR	WPI: 1990-024228/04.
XX	DR	N-PSDS; AAQ02886.
XX	PT	Placental coagulation inhibitor polypeptide -
XX	PT	having strong anticoagulation activities and obtained in large
XX	PS	amount by recombinant DNA techniques.
XX	PS	Disclosure; fig. 5; 24pp; English.
XX	CC	The polypeptide has properties similar to those of placental
XX	CC	coagulation inhibitor derived from the human placenta. It
XX	CC	can be produced in large amounts and at a low price. It has
XX	CC	strong anticoagulant activities and may be used for the
XX	CC	prevention and treatment of eg thrombosis and DIC
XX	CC	(disseminated intravascular coagulation) in the brain,
XX	CC	heart and peripheral blood vessels such as cerebral and
XX	CC	myocardial infarction. The DNA fragment encoding the CPB-II
XX	CC	polypeptide was obtained from a human placental cDNA library
XX	CC	using a CPB-II specific antibody as a probe. The DNA was
XX	CC	used to prepare a recombinant plasmid which was then used to
XX	CC	transform cells of a microorganism. See also AA03725, AAQ02887
XX	CC	and AAQ02888.
XX	CC	(Updated on 25-MAR-2003 to correct PA field.)
XX	SQ	Sequence 786 AA;

Query Match	51.1%;	Score 1708;	DB 11;	Length 786;
Best Local Similarity	51.2%;	Pfed No. 4,4e-119;		

Matches	344;	Conservative	131;	Mismatches	179;	Indels	18;	Gaps	5;
QY	12	AANKXALRGTVTDSGFDGRADAEVLKRAKMGLTDEDSILNLTARSNAORQOIAEEFKT	71						
Db	5	AOGAKYKGSIHDPFDPNODAEALYTAUKGFGSDREALIDITRSNRQREVCQYKYS	64						
QY	72	LFGRLVNDKMSLTKGFEKLYALMKPSRLDAYELKAKAGTDEKVLTEIARSTP	131						
Db	65	LYGKDLIADLKJLFTLGTFFERLIVGLMRPAYCDAKEIKOALSIGITDKCLIEIARSTN	124						
QY	132	EEIRAIKQAYEEYGSNLDDVGVDTSGYQRMVLVLLQANRDPDTAIDDAQVELDAQAL	191						
Db	125	EQHQVLAAYAKDAVEEDLEADIGDTSGHFQKMLVLLQGTREDDVVSDELVQDDVL	184						
QY	192	FOAGELKMGTDDEKFTITLIGTRSVSHLRVFDKNTISGFOIEETIDRETSGNLENLLA	251						
Db	185	YBAGEELKMGDEAQFIYILGNRSKQHLRVFGEYELTKTKPFEASIRGELSDFPHMLA	244						
QY	252	VVKSIRSIIPAYLAETLYYAMKAGTDDHTLIRIVSRSEIDLFNIRKEFRKNFATSLYSM	311						
Db	245	VVKCIRSTPEYFAERLFAKMGKLTGTDNTLIRIMVSRLDVLDRIFRTYKESLYSM	304						
QY	312	IKGDTSGDYKALLLLCGGEDDYRSR--SGLEVLFO---GPGSTYALRGTVTDFSGFD	364						
Db	305	IKNDTSGEYKKTLLKXSGGDDDAQGFPEPAQVAYQWELSAVARVELKGTVRPANDFN	364						
QY	365	GRADAEVLRKAMKGLTDEDSILNLTARSNAORQOIAEEFKTLAGRLVNDKMSLTKG	424						
Db	365	PDADAKALRKAMKGLTDEDTIIDITHSNVQRIQRTFSSHGRDMLDKSEISGD	424						
QY	425	FEKLYALMKPSRLDAYELKHAUKAGTDEKVLTEIARSTPEELRAIKQAYEEYGSN	484						
Db	425	LARLILGLMPPAHYDAKOLKAMGAGTDEKALIEILATRNALIRAINEXKYDHYKS	484						
QY	485	LEDDVVDTSIGYQRMVLVLLQANRDP---DTAIDDAQVELDAQALFOAGELKMGTD-	538						
Db	485	LEBALSDTSIGHFRRILISLATGHRBEGENLDQAREDAQV---AAETLEIADTPSGDKT	541						
QY	539	--BEKFTITLIGTRSVSHLRVFDKNTISGFOIEETIDRETSGNLENLLAVVKSIRSI	596						
Db	542	SLSTRFMTILCTRSYFHLKRVFGEFKMTNVDEHTIKKEMSGDVDAFAVALVQSVKXP	601						
QY	597	AYLAETLYYAMKAGTDDHTLIRIVSRSEIDLFNIRKEFRKNFATSLYSMTKDTSGDY	656						
Db	602	LFFADKLKXSMKAGTDEKTLIRIVSRSEIDLNIRREFIEKYKSLHQALEGTSDF	661						
QY	657	KXALLLCGGED	668						
Db	662	LKALLLCGGED	673						
RESULT 3									
AAR03725									
ID	AAR03725 standard; protein; 672 AA.								
XX	AAR03725;								
AC	AAR03725;								
DT	25-MAR-2003 (updated)								
DT	04-JUL-1990 (first entry)								
XX	Human placenta-derived coagulation inhibitor.								
XX	Human; placenta; coagulation inhibitor; anticoagulant.								
XX	Homo sapiens.								
XX	EP51826-A.								
XX	24-JAN-1990.								
XX	19-JUL-1989; 89EP-0113261.								
XX	21-JUL-1988; 88JP-0182633.								
XX									
XX	(KOMA ) KOMA CO LTD.								
XX	Iwasaki A, Suda M, Saino Y;								
XX	WPI, 1990-024228/04.								
XX	N-PSDB; AA002887.								
PT	Placental coagulation inhibitor polypeptide -								
PT	having strong anticoagulation activities and obtained in large								
PS	amount by recombinant DNA techniques.								
PS	Claim 2; page 15; 24pp; English.								
CC	The polypeptide has properties similar to those of placental								
CC	coagulation inhibitor derived from the human placenta. It								
CC	can be produced in large amounts and at a low price. It has								
CC	strong anticoagulant activities and may be used for the								
CC	prevention and treatment of eg thrombosis and DIC								
CC	(disseminated intravascular coagulation) in the brain,								
CC	heart and peripheral blood vessels such as cerebral and								
CC	myocardial infarction. The DNA fragment encoding the CPB-II								
CC	polypeptide was obtained from a human placental cDNA library								
CC	using a CPB-II specific antibody as a probe. The DNA was								
CC	used to prepare a recombinant plasmid which was then used to								
CC	transform cells of a microorganism. See also AA002887.								
CC	(updated on 25-MAR-2003 to correct PA field.)								
XX	SQ Sequence 672 AA;								
XX	Query Match 51.0%; Score 1706; DB 11; Length 672;								
XX	Best Local Similarity 51.0%; Pred. No. 5.1e-119;								
XX	Matches 343; Conservative 132; Mismatches 179; Indels 18; Gaps 5;								
QY	12	AANKXALRGTVTDSGFDGRADAEVLKRAKMGLTDEDSILNLTARSNAORQOIAEEFKT	71						
Db	4	AOGAKYKGSIHDPFDPNODAEALYTAUKGFGSDREALIDITRSNRQREVCQYKYS	63						
QY	72	LFGRLVNDKMSLTKGFEKLYALMKPSRLDAYELKHAUKAGTDEKVLTEIARSTP	131						
Db	64	LYGKDLIADLKJLFTLGTFFERLIVGLMRPAYCDAKEIKOALSIGITDKCLIEIARSTN	123						
QY	132	EEIRAIKQAYEEYGSNLDDVGVDTSGYQRMVLVLLQANRDPDTAIDDAQVELDAQAL	191						
Db	124	EQHQVLAAYAKDAVEEDLEADIGDTSGHFQKMLVLLQGTREDDVVSDELVQDDVL	183						
QY	192	FOAGELKMGTDDEKFTITLIGTRSVSHLRVFDKNTISGFOIEETIDRETSGNLENLLA	251						
Db	184	YBAGEELKMGDEAQFIYILGNRSKQHLRVFGEYELTKTKPFEASIRGELSDFPHMLA	243						
QY	252	VVKSIRSIIPAYLAETLYYAMKAGTDDHTLIRIVSRSEIDLFNIRKEFRKNFATSLYSM	311						
Db	244	VVKCIRSTPEYFAERLFAKMGKLTGTDNTLIRIMVSRLDVLDRIFRTYKESLYSM	303						
QY	312	IKGDTSGDYKALLLLCGGEDDYRSR--SGLEVLFO---GPGSTYALRGTVTDFSGFD	364						
Db	304	IKNDTSGEYKKTLLKXSGGDDDAQGFPEPAQVAYQWELSAVARVELKGTVRPANDFN	363						
QY	365	GRADAEVLRKAMKGLTDEDSILNLTARSNAORQOIAEEFKTLAGRLVNDKMSLTKG	424						
Db	364	PDADAKALRKAMKGLTDEDTIIDITRSNVQRIQRTFSSHGRDMLDKSEISGD	423						
QY	425	FEKLYALMKPSRLDAYELKHAUKAGTDEKVLTEIARSTPEELRAIKQAYEEYGSN	484						
Db	424	LARLILGLMPPAHYDAKOLKAMGAGTDEKALIEILATRNALIRAINEXKYDHYKS	483						
QY	485	LEDDVVDTSIGYQRMVLVLLQANRDP---DTAIDDAQVELDAQALFOAGELKMGTD-	538						
Db	484	LEBALSDTSIGHFRRILISLATGHRBEGENLDQAREDAQV---AAETLEIADTPSGDKT	540						
QY	539	--BEKFTITLIGTRSVSHLRVFDKNTISGFOIEETIDRETSGNLENLLAVVKSIRSI	596						
Db	541	SLSTRFMTILCTRSYFHLKRVFGEFKMTNVDEHTIKKEMSGDVDAFAVALVQSVKXP	600						





QY 477 YEEYEGSNLEDDVYDPTSGYGYRMVLVLLQANRDP-----DTAIDDAQVELDAQALFOAG 531  
 Db 485 YKEDYKSLDSDALSSDTSQGFRLTLSTATGHRESGEVLDAQEDPAQSIAT---PSG 540  
 QY 532 ELKMGTDSEKFTITLIGTSVSHLRVFPKXMTISGFQIEETIDRETSGNLENLLAVYKS 591  
 Db 541 DKT--SIETRFMTILCTRSPHLRVFOEIKMTINVDHTIKKMSGDVRAFAVALVQS 598  
 QY 592 IRSIPAYLAETLYYAMKAGTDDHTLIRVIVSRSEIDLFNIRKFRKRNFAFSLYSMIKGD 651  
 Db 599 VKNSPLFPADKLTKYMKAGTDEKTLTRIMVSHSEIDLINIRREFIEKXDSLHQALEGD 658  
 QY 652 TSGDYKKALLLLCGGED 668  
 Db 659 TSGDFLKALLALCGGED 675

## RESULT 5

ID ABP56248 standard; Protein; 319 AA.

XX ABP56248;

XX 28-MAR-2003 (first entry)

XX Human annexin V protein SEQ ID NO:3.

XX Annexin; modified; thrombosis; annexin V; thrombolytic;

XX coronary thrombosis; overt cerebral thrombosis; arterial thrombosis;

XX transient cerebral ischaemic attack; venous thrombosis.

XX Homo sapiens.

XX W0200267857-A2.

XX 06-SEP-2002.

XX 21-FEB-2002; 2002WO-US05079.

XX 21-FEB-2001; 2001US-270402P.

XX 21-NOV-2001; 2001US-332582P.

XX (SURR-) SURROMED INC.

XX Allison A;

XX WPI; 2003-129062/12.

XX N-PSDB; ABZ21925.

XX Novel isolated modified annexin proteins comprising annexin protein

XX coupled to polyethylene glycol or additional proteins, useful for

XX treating thrombosis e.g. coronary thrombosis and overt cerebral

XX thrombosis -

XX Claim 6; Page 36; 62pp; English.

XX The present invention describes a modified annexin protein (I) comprising

XX an annexin protein coupled to: (i) polyethylene glycol (PEG); or (ii) an

XX additional protein. (I) has thrombolytic activity and can be used as a

XX thrombosis modulator, and an inhibitor of cellular and humoral

XX mechanisms by which platelet aggregation is amplified. (I) can be used

XX for treating a subject at risk from thrombosis. Preferably, a

XX pharmaceutical composition comprising (I) is administered to a subject

XX after coronary thrombosis, overt cerebral thrombosis, or transient

XX cerebral ischaemic attack. More preferably, the pharmaceutical

XX SQ Sequence 319 AA;  
 Query Match 47.7%; Score 1593; DB 24; Length 319;  
 Best Local Similarity 100.0%; Pred. No. 5.5e-111;  
 Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 AIRGVTDPSSGFDGADAEVLRKAMKGLGTEDSILNLLTRSNVAORQOIAEPEKTLFGR 75  
 Db 2 AIRGVTDPSSGFDGADAEVLRKAMKGLGTEDSILNLLTRSNVAORQOIAEPEKTLFGR 61  
 QY 76 DLVNDKSELTGFEKTLVYALMKPSRLVDAYELKHAKLGAQTDEKVLTEIIASRPEELR 135  
 Db 62 DLVNDKSELTGFEKTLVYALMKPSRLVDAYELKHAKLGAQTDEKVLTEIIASRPEELR 121  
 QY 136 AIKQAYEEYEGSNLEDDVYDPTSGYGYRMVLVLLQANRDPDTAIDDAQVELDAQALFOAG 195  
 Db 122 AIKQAYEEYEGSNLEDDVYDPTSGYGYRMVLVLLQANRDPDTAIDDAQVELDAQALFOAG 181  
 QY 196 ELKMGTDSEKFTITLIGTSVSHLRVFPKXMTISGFQIEETIDRETSGNLENLLAVYKS 255  
 Db 182 ELKMGTDSEKFTITLIGTSVSHLRVFPKXMTISGFQIEETIDRETSGNLENLLAVYKS 241  
 QY 256 IRSIPAYLAETLYYAMKAGTDDHTLIRVIVSRSEIDLFNIRKFRKRNFAFSLYSMIKGD 315  
 Db 242 IRSIPAYLAETLYYAMKAGTDDHTLIRVIVSRSEIDLFNIRKFRKRNFAFSLYSMIKGD 301  
 QY 316 TSGDYKKALLLLCGGED 333  
 Db 302 TSGDFLKALLALCGGED 319

## RESULT 6

ID AAY13925 standard; Protein; 318 AA.

XX AAY13925;

XX 13-JUL-1999 (first entry)

XX S65T GFP variant/Annexin V protein.

XX GFP; green fluorescent protein; annexin; fusion protein; apoptosis;

XX fluorescent intensity; anionic phospholipid binding affinity;

XX asymmetric distribution; plasma membrane phospholipid;

XX apoptotic cell detection.

XX Aequorea victoria.

XX Synthetic.

XX W09919470-A2.

XX 22-APR-1999.

XX 09-OCT-1998; 98WO-US21444.

XX 09-OCT-1997; 97US-0948276.

XX (REGC ) UNIV CALIFORNIA.

XX Ernst JD;

XX WPI; 1999-277634/23.

XX Bifunctional fusion protein useful for the detection of apoptotic

XX cells

XX Claim 2; Page 17-18; 23pp; English.

XX This sequence represents an example of a protein of the invention.

XX The proteins are bifunctional Aequorea victoria green fluorescent protein

XX (GFP)-annexin fusion proteins, where the GFP and annexin moieties provide

CC Greater or equal fluorescent intensity and anionic phospholipid binding  
 CC affinity, respectively, than do the corresponding unfused GFP and annexin  
 CC proteins. An early manifestation of apoptosis is the loss of the  
 CC asymmetric distribution of plasma membrane phospholipids, which results  
 CC in exposure of anionic phospholipids on the extracellular leaflet of the  
 CC plasma membrane. The GFP-annexin V fusion proteins are used for the  
 CC detection of apoptotic cells by flow cytometry or fluorescent microscopy.  
 CC The fusion proteins provide for homogeneously labelled annexin, with  
 CC fluorescence properties that do not change upon binding membrane  
 CC phospholipids, unlike prior art FITC-labelled annexins, where quenching  
 CC of FITC-annexin V fluorescence by 40-50% occurs upon binding phospholipid  
 CC membranes.

XX Sequence 318 AA;

Query Match 47.3%; Score 1580; DB 20; Length 318;  
 Best Local Similarity 99.4%; Pred. No. 5.1e-110;  
 Matches 316; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 16 ALRGTVDFSGFGRADAEVLRKAMKGLGTDEDSIINLTARSNARQOIABEFTLFG 75  
 DB 1 ALRGTVDFSGFGRADAEVLRKAMKGLGTDEDSIINLTARSNARQOIABEFTLFG 60  
 QY 76 DLVNDKSELTKGFEKILVALMKPSRLYDAVELKHA KLGA GDEKVLTEIIASRTPELR 135  
 DB 61 DLVNDKSELTKGFEKILVALMKPSRLYDAVELKHA KLGA GDEKVLTEIIASRTPELR 120  
 QY 136 AIKQAEERYGSLNEDDVGDTSGYQRMVLVLLQANRPDTAIDDAQVELDAQALFQAG 195  
 DB 121 AIKQAEERYGSLNEDDVGDTSGYQRMVLVLLQANRPDTAIDDAQVELDAQALFQAG 180  
 QY 196 ELKMGTEDEKFTILIGTRSVSHLRVPDKYMTISGQIETITRETSNLENLLAVK 255  
 DB 181 ELKMGTEDEKFTILIGTRSVSHLRVPDKYMTISGQIETITRETSNLENLLAVK 240  
 QY 256 IRSIPAYLAETLYYAMKAGTDDHTLIRIVSRSEIDLFNIRKEFRKNFATSLYSMTKGD 315  
 DB 241 IRSIPAYLAETLYYAMKAGTDDHTLIRIVSRSEIDLFNIRKEFRKNFATSLYSMTKGD 300  
 QY 316 TSGDYKKALLLCCGEDD 333  
 DB 301 TSGDYKKALLLCCGEDD 318

RESULT 7

AAR75695  
 ID AAR75695 standard; peptide; 319 AA.

XX AAR75695;

DT 21-JAN-1996 (first entry)

XX Rat annexin-V.

KM Amyloid precursor protein; APP; annexin-V; Alzheimer's disease;  
 KW disease diagnosis; therapy; antibody.

OS Rattus rattus.

XX Key Location/Qualifiers

FT Peptide 57..68

FT Peptide 85..95

FT Peptide 107..120

FT Peptide 259..284

XX EP655626-A1.

XX 31-MAY-1995.

PF 10-NOV-1994; 94EP-0308309.

PR 10-NOV-1993; 93US-0149975.

XX

PA (MCLE-) MCLEAN HOSPITAL CORP.

PI Honda T, Nixon R;

XX WPI; 1995-195688/26.

XX New peptide(s) associated with Alzheimer's disease - namely p33 and

PT the amyloid precursor C2 fragment, useful for the prodn. of

XX diagnostic antibodies

PS Disclosure; Fig.9; 32pp; English.

CC This amino acid sequence is contained within the 33 kDa protein  
 CC (p33) sequence and the indicated peptides are produced following  
 CC lysyl-endopeptidase cleavage of p33. Detection and quantification  
 CC of this protein is therefore useful for diagnosing the disease.

SO Sequence 319 AA;

Query Match 47.0%; Score 1570; DB 16; Length 319;  
 Best Local Similarity 98.7%; Pred. No. 2.9e-109;  
 Matches 314; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 16 ALRGTVDFSGFGRADAEVLRKAMKGLGTDEDSIINLTARSNARQOIABEFTLFG 75  
 DB 2 ALRGTVDFSGFGRADAEVLRKAMKGLGTDEDSIINLTARSNARQOIABEFTLFG 61  
 QY 76 DLVNDKSELTKGFEKILVALMKPSRLYDAVELKHA KLGA GDEKVLTEIIASRTPELR 135  
 DB 62 DLVNDKSELTKGFEKILVALMKPSRLYDAVELKHA KLGA GDEKVLTEIIASRTPELR 121  
 QY 136 AIKQAEERYGSLNEDDVGDTSGYQRMVLVLLQANRPDTAIDDAQVELDAQALFQAG 195  
 DB 122 AIKQAEERYGSLNEDDVGDTSGYQRMVLVLLQANRPDTAIDDAQVELDAQALFQAG 181  
 QY 196 ELKMGTEDEKFTILIGTRSVSHLRVPDKYMTISGQIETITRETSNLENLLAVK 255  
 DB 182 ELKMGTEDEKFTILIGTRSVSHLRVPDKYMTISGQIETITRETSNLENLLAVK 241  
 QY 256 IRSIPAYLAETLYYAMKAGTDDHTLIRIVSRSEIDLFNIRKEFRKNFATSLYSMTKGD 315  
 DB 242 IRSIPAYLAETLYYAMKAGTDDHTLIRIVSRSEIDLFNIRKEFRKNFATSLYSMTKGD 301  
 QY 316 TSGDYKKALLLCCGEDD 333  
 DB 302 TSGDYKKALLLCCGEDD 319

RESULT 8

ABG19948  
 ID ABG19948 standard; Protein; 736 AA.

XX ABG19948;

DT 18-FEB-2002 (first entry)

XX Novel human diagnostic protein #19939.

KM Human; chromosome mapping; gene therapy; forensic;  
 KW food supplement; medical imaging; diagnostic; genetic disorder.

OS Homo sapiens.

XX WO200175067-A2.

XX 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US08631.

PR 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

PA (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;  
 XX WPI, 2001-639362/73.  
 DR N-PSDB; AAS84135.  
 XX New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity -  
 XX Claim 20; SEQ ID No 50307; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and  
 CC polypeptide (II) sequences (I) is useful as hybridization probes,  
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
 CC and gene mapping, and in recombinant production of (II). The  
 CC polynucleotides are also used in diagnostics as expressed sequence tags  
 CC for identifying expressed genes. (I) is useful in gene therapy techniques  
 CC to restore normal activity of (II) or to treat disease states involving  
 CC (II). (II) is useful for generating antibodies against it, detecting or  
 CC quantitating a polypeptide in tissue, as molecular weight markers and as  
 CC a food supplement. (II) and its binding partners are useful in medical  
 CC imaging of sites expressing (II). (I) and (II) are useful for treating  
 CC disorders involving aberrant protein expression or biological activity.  
 CC The polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations in  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. AAG00010-AAG03037 represent novel human  
 CC diagnostic amino acid sequences of the invention.  
 CC Note: The sequence data for this patent did not appear in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 736 AA:

Query Match 46.6%; Score 1558; DB 22; Length 736;  
 Best Local Similarity 49.4%; Pred. No. 6,4e-108;  
 Matches 331; Conservative 127; Mismatches 188; Indels 24; Gaps 11;

QY 18 RGVTPDPSGPDGRADDEVLRKAMKGLGDESDSILNLTPASNAQOQAEFKTLFGRDL 77  
 Db 70 RGSIDHPGPDNPQDEALYIMKGGSKKALDITTSRNRQSQEGCHSKYKSLYKDL 129  
 QY 78 VDMKSELGKEFKLVALMKPSRLYAYELKAKLGAGDEKVTETIASRTEEL-RA 136  
 Db 130 IADLKVELGKFERLIVLRMRPVCDAKEIKDAISGIGTEKCEILIASRTNEQHQL 169  
 QY 137 IKQAYEEYGSNIEDDVGDTSYQRMVLVLLQANRDPDAIDAOVELDAQLFOAGE 196  
 Db 190 VKRITMPTERLEADIIIDTSGHFQKMLVLLQGTREDDVVSDDVQVQDLVEAGE 249  
 QY 197 LKMGDEKEFTITLIGRSVSHLRVFDKMTISGQFETIDRETSGLLELLAAVKS 256  
 Db 250 LKMGDEAGQFIVILGSRKQHLVDFDELTKTGFRASIRGELSGDFELMLAAVKCI 309  
 QY 257 RSLPAYLAETLYYANKAGATDHTLIRIVVSRSEIDLFNIRKFRKFA-TSLYSK-IGK 314  
 Db 310 RSTPEYFAERLFRAMKGLGTRDNTLIRIVVSRSEIDMDIREIFRTYXKESLSMIDKN 369  
 QY 315 DTSG-DYKALLLLCGGEDDXRSR---SGLEVLFO---GGSTXALRGVTIDPSGPDGR 366  
 Db 370 DTSGGSKYKTLTKLTSGEDDADQFPKRAQVAYQMLSAVAYELKGVIRPANDNPD 429  
 QY 367 ADAEVLKAMKGLGDESDSILNLTPASNAQOQAEFKTLFGRDLVDMKSELGKFE 426  
 Db 430 ADAKALRKAMKGLGDESDSILNLTPASNAQOQAEFKTLFGRDLVDMKSELGKFE 426  
 QY 427 KLIIVALKPSRLYDAELKALCGAGTDEKVTETIASRTEELRAIKQAYEEYGSNLE 466  
 Db 490 RLILGLMPPPAHYDAKOLKRAKMEGAGTEKALIEILATRTNAEIRAINAEAYKEDYHKSLE 549

QY 487 DDVGDTSYQRMVLVLLQANRDP-----DTAIDAOVELDAQLFOAGELKMGTD--- 538  
 Db 550 DALSDSTGSHFRRLIISLATGHRREGENDQANEDQAV---AAEILIEIDPTSGKTSI 606  
 QY 539 EEKFTTIGTSVSHLRVFDKMTISGQFETIDRETSGLLELLAAVKSIRISIPAY 598  
 Db 607 EIRFMTICTSYHVRVRIQFIRLNVQVEHRTKEMSGDIRDAFVAIVGSAKRPLE 666  
 QY 599 LAETLYYANKAGATDHTLIRIVVSRSEIDLFNIRKFR-KNPAISLYSNIKG-DTSGDY 656  
 Db 667 FPDKLYKSKAGAGTDEKTLIRIVVSRSEIDLINIRGIPRIEKDKSIHQIXGXTTQGF 726  
 QY 657 KXALLLGGG 666  
 Db 727 LKALPACGG 736

RESULT 9  
 ID AAY13924 standard; protein; 319 AA.  
 XX AAY13924;  
 AC AAY13924;  
 DT 13-JUL-1999 (first entry)  
 XX 565T GFP variant/hAnnexin V protein.  
 DE GFP, green fluorescent protein; annexin, fusion protein; apoptosis;  
 KM fluorescent intensity; anionic phospholipid binding affinity;  
 KW asymmetric distribution; plasma membrane phospholipid;  
 KM apoptotic cell detection.  
 XX Aequorea victoria.  
 OS Homo sapiens.  
 OS Synthetic.  
 PN WO9319470-A2.  
 XX 22-APR-1999.  
 PD 09-OCT-1998; 98WO-US21444.  
 PF 09-OCT-1997; 97US-0948276.  
 PR (REGC) UNIV CALIFORNIA.  
 XX Ernst JD;  
 XX WPI, 1999-277634/23.  
 DR Bifunctional fusion protein useful for the detection of apoptotic  
 PT cells  
 PT Claim 2; Page 15-17; 23pp; English.  
 PS This sequence represents an example of a protein of the invention.  
 CC The proteins are bifunctional Aequorea victoria green fluorescent protein  
 CC (GFP)-annexin fusion proteins, where the GFP and annexin moieties provide  
 CC greater or equal fluorescent intensity and anionic phospholipid binding  
 CC affinity, respectively, than do the corresponding unfused GFP and annexin  
 CC proteins. An early manifestation of apoptosis is the loss of the  
 CC asymmetric distribution of plasma membrane phospholipids, which results  
 CC in exposure of anionic phospholipids on the extracellular leaflet of the  
 CC plasma membrane. The GFP-annexin V fusion proteins are used for the  
 CC detection of apoptotic cells by flow cytometry or fluorescent microscopy.  
 CC The fusion proteins provide for homogeneously labelled annexin, with  
 CC fluorescence properties that do not change upon binding membrane  
 CC phospholipids, unlike prior art FITC-labelled annexins, where quenching  
 CC of FITC-annexin V fluorescence by 40-50% occurs upon binding phospholipid  
 CC membranes.  
 XX Sequence 319 AA;

Query Match	45.8%	Score 1530	DB 20	Length 319
Best Local Similarity	95.3%	Pred. No. 2,8e-106		
Matches 303	Conservative 7	Mismatches 8	Indels 0	Gaps 0
QY	16	ALRGVTVDFSGFDGRADAEVLKPAKKGAGTDEDSILNLTARSNAORQIAEFKTLFGR	75	
Db	2	ATRGVTVDFGFGGRADAEVLKPAKKGAGTDEDSILNLTARSNAORQIAEFKTLFGR	61	
QY	76	DLYNDKSELTGFEFLIYALMKPSRLIDAYELKAKLGAGTDEKVTETIISRTPEELR	135	
Db	62	DLYNDKSELTGFEFLIYAMMKPSRLIDAYELKAKLGAGTDEKVTETIISRTPEELR	121	
QY	136	AIKQAYEEBYGSNLIEDVVGPTSGYYGNLVLLQANRDPITALDQAYLDAQALFQK	195	
Db	122	AIKQAYEEBYGSNLIEDVVGPTSGYYGNLVLLQANRDPITALDQAYLDAQALFQK	181	
QY	196	ELKMGVDEDEKFTIILCTRSVSHLRVFPKXTYISGQIESTIDERTSGNLEMLLAVKS	255	
Db	182	ELKMGVDEDEKFTIIFGTRSVSHLRVFPKXTYISGQIESTIDERTSGNLEMLLAVKS	241	
QY	256	IRSLPAYIAETLYYAKKGAGTDPHTLIIVYSRSEIDLFNIRKFRNFRNFTSLYSIKRD	315	
Db	242	IRSLPAYIAETLYYAKKGAGTDPHTLIIVYSRSEIDLFNIRKFRNFRNFTSLYSIKRD	301	
QY	316	TSGDYKALLLLLCGGEDD 333		
Db	302	TSGDYKALLLLLCGGEDD 319		
RESULT 10				
ABB57067				
ID	ABB57067	standard; Protein; 319 AA.		
AC	ABB57067;			
XX				
DT	07-MAR-2002	(first entry)		
XX				
DE	Mouse ischaemic condition related protein sequence SEQ ID NO:136.			
XX				
KW	Mouse; Ischaemia; compressive ischaemia; occlusive ischaemia;			
XX	vasospastic ischaemia; ischaemic condition; ischaemic disease.			
OS	Mus musculus.			
XX				
PN	W0200183188-A2.			
XX				
PD	22-NOV-2001.			
XX				
PF	18-MAY-2001; 2001WO-0P04192.			
XX				
PR	18-MAY-2000; 2000CP-0145977.			
XX				
PA	(UTN1-) UNIV NITHON SCHOOL JURIDICAL PERSON.			
PI	Ishikawa K, Arai S, Takahashi Y, Nagata T, Ishii Y;			
XX				
DR	WPI: 2002-034733/04.			
XX				
DR	N-PSDB; ABI95289.			
XX				
PS	Claim 2; Page 419-421; 2690pp; English.			
XX				
CC	The present invention describes a method for examining ischaemic			
XX	conditions, comprising measuring the expression levels of particular			
CC	genes (I) in a test sample or determining the expression profile of a			
XX	gene group in the sample comprising genes selected from (I). The method			
CC	is useful for examining the ischaemic condition (e.g. compressive			
XX	ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring			
CC	expression levels of particular genes (ABI95202 to ABI95912, encoding			

CC	the protein sequences in AB57020 to AB57374) or by determining the
CC	expression profile of a gene group comprising these genes. The
CC	expression levels or expression profiles produced by these genes are
CC	used as an indicator when screening for ischaemic condition-improving
CC	drugs or antidiabetics for ischaemic diseases. AB199313 and AB199314
CC	represent PCR primers for a mouse ischaemic condition related sequence,
CC	which are used in the exemplification of the present invention.
XX	
SQ	Sequence 319 AA;
Query Match	45.8%; Score 1530; DB 23; Length 319;
Best Local Similarity	95.3%; Pred. No. 2.8e-106;
Matches 303; Conservative 7; Mismatches 8; Indels 0; Gaps 0	
Dy	16 ALRGVLTDSGFGADAEVLKAKKGIGTDEDSILNLTARSNAORQQIAEERKTLFGR 75
Dd	2 ATAGVTDPGGDGRADAEVLKAKKGIGTDEDSILNLTARSNAORQQIAEERKTLFGR 61
Dy	76 DLVNMDKSELGTGFELIVAMKPSRLDAYVELKHAKLGAGTDKCVLTEIIASRPEELR 135
Dd	62 DLVDDLKSELTGFEFLIVAMKPSRLDAYVELKHAKLGAGTDKCVLTEIIASRPEELS 121
Dy	136 AITQAVEERYSGNLBDVDYDTISGYQMLVYLQANRPDTAIDDAQVEIDAQALFOAG 195
Dd	122 AITQAVEERYSGNLBDVDYDTISGYQMLVYLQANRPDTAIDDAQVEIDAQALFOAG 181
Dy	196 ELKMGTDERKFTIIGTSVSLSLRVPFKMTISGFOIEETIDRETSGNLELLAVYS 255
Dd	182 ELKMGTDERKFTIIGTSVSLSLRVPFKMTISGFOIEETIDRETSGNLEQLLAVYS 241
Dy	256 IRSIPAYLAETLYVANKGATDHTLLNVIVSRSEIDLFNIRKEFRKNPATSIVSMIKGD 315
Dd	242 IRSIPAYLAETLYVANKGATDHTLLRVVSRSEIDLFNIRKEFRKNPATSIVSMIKGD 301
Dy	316 TSGDYKKALLLLCGGEDD 333
Dd	302 TSGDYKKALLLLCGGEDD 319
RESULT 11	
ID	AA932930
AA932930	standard; Protein; 600 AA.
AC	AA932930;
XX	
XX	25-OCT-2000 (first entry)
XX	
DE	Annexin V/uropkinase fusion protein.
XX	
KM	Annexin V; thrombocyte; carrier; thrombus; thrombolytic; fusion protein;
KW	urokinase; insect cell; fibrinolysis.
XX	
OS	Unidentified.
NN	CNI247195-A.
PD	15-MAR-2000.
PF	12-MAR-1999; 99CN-0113524.
PR	12-MAR-1999; 99CN-0113524.
PA	(SHAN-) SHANGHAI INST BIOCHEMISTRY CHINESE ACAD.
PI	Wu X, Sun J, Yang G;
DR	WPJ; 2000-413098/36.
DR	N-PSDB; AAA11241.
PT	New thrombolytic fusion protein for targeting thrombus - comprises
PT	fusion of Annexin V and urokinase
SS	Claim 2; Page 2-4; 20pp; Chinese.

XX Annexin V, which has high affinity for active thrombocytes, is used  
 CC as a carrier molecule to build a thrombus-targeting thrombolytic fusion  
 CC protein. The protein (this sequence) is the result of expression of a  
 CC fusion gene comprising the Annexin V gene and a low-molecular urokinase  
 CC gene, in insect cells. The Annexin V-scu-PA-32 fusion protein, expressed  
 CC in insect cell strain Tn-531-4, has high affinity for active thrombocytes  
 CC and has the fibrinolytic activity of urokinase.

XX Sequence 600 AA:

Query Match 43.4%; Score 1452.5; DB 21; Length 600;  
 Best Local Similarity 87.3%; Pred. No. 3.7e-100;  
 Matches 290; Conservative 18; Mismatches 23; Indels 1; Gaps 1;

QY 2 DYKDDDDKLAANAALRGIVTDFSGPDGADAEVLRKAKGIGTDEDSITLNLTRASNAQ 61  
 DB 270 DFEIPEEYEVAAQVLRGTLTDFPGFDERADAEIRKAKGIGTDEESITLTLRSNAQ 329  
 QY 62 RQIAIEEFKTLFGRLDNDKSELGKFEKLIYALMKPSRLYDAYELKHALGAGTDEKV 121  
 DB 330 RQISAAFKTLFGRLDNDKSELGKFEKLIYALMKPSRLYDAYELKHALGAGTDEKV 389  
 QY 122 LFTIISRTPEELRAIKQAYEEYSGNLDDVVGDTSGYQRMVLVLLQANRDPDAID 181  
 DB 390 LFTIISRTPEELRAIKQAYEEYSGNLDDVVGDTSGYQRMVLVLLQANRDPDAID 449  
 QY 182 AQVELDAQALFOAGELKMGTDDEKFTITLGRSVSHLRVFPDKMTISGFOIETIDRET 241  
 DB 450 AQVELDAQALFOAGELKMGTDDEKFTITLGRSVSHLRVFPDKMTISGFOIETIDRET 509  
 QY 242 SGNLENLLAVVKSIRSIIPAYLAETLYYAMKAGTDDHTLIRVRSSEIDLFNIRKEFR 301  
 DB 510 SGNLEQLLAVVKSIRSIIPAYLAETLYYAMKAGTDDHTLIRVRSSEIDLFNIRKEFR 569  
 QY 302 KNPATSLYSMIKGDTSGDYKALLLCCGEDD 333  
 DB 570 KNPATSLYSMIKGDTSGDYKALLLCCGEDD 600

# RESULT 12

AAR26276 standard; protein, 319 AA.

XX AAR26276;  
 AC 10-MAR-2003 (updated)  
 DT 04-FEB-1993 (first entry)  
 XX CPB-I.  
 XX CPB-I; stabilisation; frozen; molten; processed; activity.  
 XX Homo sapiens.  
 OS JP04198195-A.  
 PN 17-JUL-1992.  
 PD 28-NOV-1990; 90JP-0328286.  
 PF 28-NOV-1990; 90JP-0328286.  
 PR 28-NOV-1990; 90JP-0328286.  
 XX (KAGA) KAGAKU OYOBI KESSEI RYOHO.  
 PA (KOMA) KOMA CO LTD.  
 DR WPI; 1992-288937/35.  
 XX Stabilisation of CPB-I for drug compn. - by adding basic  
 PT aminoacid selected from lysine, arginine and/or ornithine  
 XX Disclosure; Page 2, 4pp; Japanese.

CC The sequence given is the amino acid sequence of CPB-I. CPB-I was  
 CC used within a method which involved adding basic amino acids to it  
 CC which resulted in its stabilisation. This lead to the production of  
 CC CPB-I which keeps its activity when it is frozen, molten or has been  
 CC processed by several procedures.  
 CC (updated on 10-MAR-2003 to add missing OS field.)

XX Sequence 319 AA:

Query Match 43.4%; Score 1451.5; DB 13; Length 319;  
 Best Local Similarity 91.5%; Pred. No. 2e-100;  
 Matches 290; Conservative 12; Mismatches 14; Indels 1; Gaps 1;

QY 17 LRGITDPSGPDGADAEVLRKAKGIGTDEDSITLNLTRASNAQRIAEKTLFGRLD 76  
 DB 4 LRGITDPSGPDGADAEVLRKAKGIGTDEESITLTLRSNAQRIAEKTLFGRLD 63  
 QY 77 LVNDKSELGKFEKLIYALMKPSRLYDAYELKHALGAGTDEKVLTEIISRTPEELRA 136  
 DB 64 LVNDKSELGKFEKLIYALMKPSRLYDAYELKHALGAGTDEKVLTEIISRTPEELRA 123  
 QY 137 IKQAYEEYSGNLDDVVGDTSGYQRMVLVLLQANRDPDAIDDAQVELDAQALFOAG 196  
 DB 124 IKQAYEEYSGNLDDVVGDTSGYQRMVLVLLQANRDPDAIDDAQVELDAQALFOAG 183  
 QY 197 LKMGTDDEKFTITLGRSVSHLRVFPDKMTISGFOIETIDRETSGNLENLLAVVKS 256  
 DB 184 LKMGTDDEKFTITLGRSVSHLRVFPDKMTISGFOIETIDRETSGNLENLLAVVKS 243  
 QY 257 RSIPAYLAETLYYAMKAGTDDHTLIRVRSSEIDLFNIRKEFRKNPATSLYSMIKGD 316  
 DB 244 RSIPAYLAETLYYAMKAGTDDHTLIRVRSSEIDLFNIRKEFRKNPATSLYSMIKGD 303  
 QY 317 SGNLEQLLAVVKSIRSIIPAYLAETLYYAMKAGTDDHTLIRVRSSEIDLFNIRKEFR 333  
 DB 304 SGNLEQLLAVVKSIRSIIPAYLAETLYYAMKAGTDDHTLIRVRSSEIDLFNIRKEFR 319

# RESULT 13

AAR41021 standard; protein, 319 AA.

XX AAR41021;  
 AC 29-MAR-1994 (first entry)  
 DT Calphobindin I (CPB-I).  
 XX Calphobindin I; CPB-I; Protein kinase C; PKC; inhibition; tumour.  
 XX Homo sapiens.  
 OS JP05213769-A.  
 PN 24-AUG-1993.  
 PD 04-FEB-1992; 92JP-0019032.  
 PF 04-FEB-1992; 92JP-0019032.  
 PR 04-FEB-1992; 92JP-0019032.  
 XX (KAGA-) ZH KAGAKU OYOBI KESSEN RYOHO KENKYUSHO.  
 PA WPI; 1993-299558/38.  
 DR Protein kinase C inhibitor effective against malignant tumours -  
 PT contg. (opt. recombinant) calphobindin I  
 XX Claim 1; Page 2-3; 6pp; Japanese.  
 CC Calphobindin I (CPB-I) or recombinant calphobindin I (r-CPB-I)  
 CC inhibits protein kinase C (PKC) and is useful in the treatment of  
 CC malignant tumours caused by abnormal activation of PKC. CPB-I is

CC extracted from human or animal organs and may be applied  
 CC intravenously, orally, intramuscularly, percutaneously or rectally.  
 XX  
 SQ Sequence 319 AA;

Query Match 43.4%; Score 1451.5; DB 14; Length 319;  
 Best Local Similarity 91.5%; Pred. No. 2e-100;  
 Matches 290; Conservative 12; Mismatches 14; Indels 1; Gaps 1;

QY 17 LRGTVDPSGFGDADAEVLKAMKGLGTEDESLINLLTSSNAQROQIAEERKTLFGRD 76  
 DB 4 LRGTVDPSGFGDADAEVLKAMKGLGTEDESLINLLTSSNAQROQIAEERKTLFGRD 63  
 QY 77 LVNDKSELTGKFEKTLVALLMPKPSRLYDAVELKAKLGAQDEKVTETIASRPEELRA 136  
 DB 64 LDDDKSELTGKFEKTLVALLMPKPSRLYDAVELKAKLGAQDEKVTETIASRPEELRA 123  
 QY 137 IKQAYEEYGSNLEDDVVDGTSGYQRMVLVLLQANRDPDAIDDAQVELDAQALFQAGE 196  
 DB 124 IKQAYEEYGSNLEDDVVDGTSGYQRMVLVLLQANRDPDAIDDAQVELDAQALFQAGE 183  
 QY 197 LKMGTEDEKFTITIGTSVSHLRVPDKYMTISGQIEETIDRETSGNLELLAVVKS 256  
 DB 184 LKMGTEDEKFTITIGTSVSHLRVPDKYMTISGQIEETIDRETSGNLELLAVVKS 243  
 QY 257 RSIPAYLAETLYYAMKAGTDHDTLIRVIVSRSEIDLFRNKEFRKNFATSLYSMTKGD 316  
 DB 244 RSIPAYLAETLYYAMKAGTDHDTLIRVIVSRSEIDLFRNKEFRKNFATSLYSMTKGD 303  
 QY 317 SGDYKRALLLCGEED 333  
 DB 304 SGDYKRALLLCGEED 319

#### RESULT 14

ABG32550  
 ID ABG32550 standard; protein; 319 AA.

XX AC ABG32550;  
 XX DT 29-NOV-2002 (first entry)  
 XX DE Human CPB-1 protein.  
 XX KW Human; CPB-1; eye drop; ophthalmological; aneixin V; corneal disease;  
 XX KW calcium/phospholipid binding protein; polyhydric alcohol.  
 XX OS Homo sapiens.  
 XX PN WO200267977-A1.  
 XX PD 06-SEP-2002.  
 XX PF 21-FEB-2002; 2002WO-JP01563.  
 XX PR 26-FEB-2001; 2001JP-0050297.  
 XX PA (KOWA) KOWA CO LTD.  
 XX PA (KAGA) CHEMO-SERO-THERAPEUTIC RES INST.  
 XX PI Naruse H, Sano M, Shinoda Y, Inagi T;  
 XX WPI; 2002-674988/72.  
 XX DR Eye drops for treating e.g. corneal diseases, contain CPB-1 and  
 XX PT polyhydric alcohol with specific carbonyl value, without unpleasant  
 XX PT irritation upon dropping but with satisfactory long-term storability  
 XX XX Disclosure; Page 13-14; 16pp; Japanese.  
 CC The invention relates to eye drops contain CPB-1 (aneixin V) and a  
 CC polyhydric alcohol having a carbonyl value of not more than  
 CC 5micro Mol /g. The eyes drops are for treating e.g. corneal diseases.

CC Such eye drops are without unpleasant irritation upon dropping but with  
 CC satisfactory long-term storage stability. The present sequence is  
 CC the human CPB-1 (calcium/phospholipid binding) protein.  
 XX  
 SQ Sequence 319 AA;

Query Match 43.4%; Score 1451.5; DB 23; Length 319;  
 Best Local Similarity 91.5%; Pred. No. 2e-100;  
 Matches 290; Conservative 12; Mismatches 14; Indels 1; Gaps 1;

QY 17 LRGTVDPSGFGDADAEVLKAMKGLGTEDESLINLLTSSNAQROQIAEERKTLFGRD 76  
 DB 4 LRGTVDPSGFGDADAEVLKAMKGLGTEDESLINLLTSSNAQROQIAEERKTLFGRD 63  
 QY 77 LVNDKSELTGKFEKTLVALLMPKPSRLYDAVELKAKLGAQDEKVTETIASRPEELRA 136  
 DB 64 LDDDKSELTGKFEKTLVALLMPKPSRLYDAVELKAKLGAQDEKVTETIASRPEELRA 123  
 QY 137 IKQAYEEYGSNLEDDVVDGTSGYQRMVLVLLQANRDPDAIDDAQVELDAQALFQAGE 196  
 DB 124 IKQAYEEYGSNLEDDVVDGTSGYQRMVLVLLQANRDPDAIDDAQVELDAQALFQAGE 183  
 QY 197 LKMGTEDEKFTITIGTSVSHLRVPDKYMTISGQIEETIDRETSGNLELLAVVKS 256  
 DB 184 LKMGTEDEKFTITIGTSVSHLRVPDKYMTISGQIEETIDRETSGNLELLAVVKS 243  
 QY 257 RSIPAYLAETLYYAMKAGTDHDTLIRVIVSRSEIDLFRNKEFRKNFATSLYSMTKGD 316  
 DB 244 RSIPAYLAETLYYAMKAGTDHDTLIRVIVSRSEIDLFRNKEFRKNFATSLYSMTKGD 303  
 QY 317 SGDYKRALLLCGEED 333  
 DB 304 SGDYKRALLLCGEED 319

#### RESULT 15

AAP80511  
 ID AAP80511 standard; protein; 320 AA.

XX AC AAP80511;  
 XX DT 25-MAR-2003 (updated)  
 XX DT 10-MAR-2003 (updated)  
 XX DT 12-NOV-1990 (first entry)  
 XX DE Placental coagulation inhibitor.  
 XX KW Placental coagulation inhibitor; disseminated vascular coagulation;  
 XX KW thrombosis.  
 XX OS Homo sapiens.  
 XX PN EP279459-A.  
 XX PN JP03219875-A.  
 XX PD 24-AUG-1988.  
 XX PF 19-FEB-1988; 88EP-0102468.  
 XX PR 20-FEB-1987; 87JP-0037227.  
 XX PR 23-JUL-1987; 87JP-0184428.  
 XX PA (KOWA) KOWA CO LTD.  
 XX PI Saito Y, Iwasaki A, Suda M;  
 XX WPI; 1988-236733/34.  
 XX WPI; 1991-329110/45.  
 XX N-PSDB; AAN81113.  
 XX DR Recombinant placental coagulation inhibitor - useful for the prevention  
 XX PT and treatment of thromboses or disseminated intra-vascular coagulation.

PS Disclosure; Page 2; 7pp; English.

XX  
CC This polypeptide exhibits strong anticoagulant activities and is useful  
CC for the treatment and prevention of e.g. thrombosis or disseminated  
CC intravascular coagulation in the brain, heart and peripheral blood  
CC vessels, such as cerebral and myocardial infarction. It has no  
CC antigenicity against man and can be produced in large amounts using  
CC recombinant methods.  
CC (Updated on 10-MAR-2003 to add missing OS field.)  
CC (Updated on 25-MAR-2003 to correct PR field.)  
CC (Updated on 25-MAR-2003 to correct PR field.)  
CC (Updated on 25-MAR-2003 to correct PA field.)  
XX  
SQ Sequence 320 AA;

Query Match 43.4%; Score 1451.5; DB 9; Length 320;

Best Local Similarity 91.5%; Pred. No. 2e-100;  
Matches 290; Conservative 12; Mismatches 14; Indels 1; Gaps 1;

QY	17	LRGTVDPSGFDGRADAEVLRKAMKGLGTDDESIINLLTARSNAORQIAEFKTLFGRD	76
Db	5	LRGTVDPSGFDGRADAEVLRKAMKGLGTDDESIINLLTARSNAORQISAFKTLFGRD	64
QY	77	LVDKSELTGKFEKLIVALMKPSRLYDAYEELKAKLAGTDEKVLTIISRTPEELRA	136
Db	65	LVDKSELTGKFEKLIVALMKPSRLYDAYEELKAKLAGTDEKVLTIISRTPEELRA	124
QY	137	IKOAYEEEGSNLEDDVVDGTSYVORMVLLQANRDPDAIDDAQVELDAQALFOAGE	196
Db	125	IKQVDEEYGSLEDDVVDGTSYVORMVLLQANRDPDAIDDAQVELDAQALFOAGE	184
QY	197	LKMGTDDEKFIITLGRSVSHLRVVDKMYTISGFQIETIDRETSGNLEMLLAVYSI	256
Db	185	LKMGTDDEKFIITLGRSVSHLRVVDKMYTISGFQIETIDRETSGNLEMLLAVYSI	244
QY	257	RSTPAYLAETLYAMKAGTDHTLIRVVSSEIDLPIRKEFRKNPATSLYSNIKGD	316
Db	245	RSTPAYLAETLYAMKAGTDHTLIRVVSSEIDLPIRKEFRKNPATSLYSNIKGD	304
QY	317	SGDYKXALLLLCGEDD	333
Db	305	SGDYKXALLLLC-GEED	320

Search completed: December 12, 2003, 14:50:03  
Job time : 53.1387 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 12, 2003, 14:50:08 ; Search time 37.2419 Seconds

(without alignments) 3340.943 Million cell updates/sec

Title: PCT-US03-24332-6

Perfect score: 3343

Sequence: 1 MDYKDDDDKLAANXALRGT.....GDTSGDYKKALLLCGHRD 669

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 684280 seqs, 185983659 residues

Total number of hits satisfying chosen parameters: 684280

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*

2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*

3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*

4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep:\*

5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep:\*

6: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*

7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*

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9: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*

10: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*

11: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB.pep:\*

12: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep:\*

13: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep:\*

14: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep:\*

15: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep:\*

16: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*

17: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep:\*

18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3337	99.8	669	12 US-10-080-370-6	Sequence 6, Appl1
2	1593	47.7	319	12 US-10-080-370-3	Sequence 3, Appl1
3	1451.5	43.4	320	14 US-10-007-761-72	Sequence 72, Appl1
4	1442.5	43.1	327	10 US-09-970-969-2	Sequence 2, Appl1
5	1442.5	43.1	327	10 US-09-970-969-4	Sequence 4, Appl1
6	1442.5	43.1	327	10 US-09-970-969-6	Sequence 6, Appl1
7	921	27.6	321	15 US-10-097-340-10	Sequence 10, Appl1
8	921	27.6	324	9 US-09-925-301-1062	Sequence 1062, App
9	887	26.5	208	9 US-09-925-302-731	Sequence 731, App
10	822.5	24.6	327	12 US-10-236-031B-18	Sequence 18, Appl1
11	790	23.6	324	12 US-10-316-253-262	Sequence 262, App
12	785	23.5	323	15 US-10-205-823-34	Sequence 34, Appl1
13	763.5	22.8	465	10 US-09-925-300-1664	Sequence 1664, App
14	695.5	20.8	339	10 US-09-974-258-91	Sequence 91, Appl1
15	695.5	20.8	339	15 US-10-097-340-6	Sequence 6, Appl1

16	695.5	20.8	339	15 US-10-097-340-8	Sequence 8, Appl1
17	678	20.3	327	9 US-09-764-853-615	Sequence 615, App
18	675	20.2	332	11 US-09-764-881-110	Sequence 110, App
19	647.5	19.4	319	15 US-10-304-287-2	Sequence 2, Appl1
20	632	18.9	373	9 US-09-925-301-888	Sequence 888, App
21	628	18.8	346	10 US-09-919-172-39	Sequence 39, Appl1
22	628	18.8	346	10 US-09-974-298-93	Sequence 93, Appl1
23	625	18.7	346	10 US-09-316-253-300	Sequence 300, App
24	381.5	11.4	289	9 US-09-925-301-897	Sequence 897, App
25	376.5	11.3	316	15 US-10-219-220-260	Sequence 260, App
26	374.5	11.2	316	15 US-10-219-220-62	Sequence 62, Appl1
27	316	9.5	158	9 US-09-925-297-479	Sequence 479, App
28	237.5	7.1	239	15 US-10-219-220-65	Sequence 65, Appl1
29	223.5	6.7	319	12 US-10-259-165-56	Sequence 56, Appl1
30	223.5	6.7	319	12 US-10-259-165-402	Sequence 402, App
31	222	6.6	336	12 US-10-259-165-290	Sequence 290, App
32	221	6.6	184	15 US-10-219-220-66	Sequence 66, Appl1
33	147.5	4.4	701	9 US-09-815-242-13002	Sequence 13002, A
34	141	4.2	82	9 US-09-925-301-1467	Sequence 1467, Ap
35	131	3.9	617	9 US-09-815-242-5762	Sequence 5762, Ap
36	130.5	3.9	1786	10 US-09-712-096-3	Sequence 3, Appl1
37	129	3.9	872	14 US-10-047-260-38	Sequence 38, Appl1
38	127.5	3.8	1004	10 US-09-738-626-5676	Sequence 5676, Ap
39	127.5	3.8	1007	11 US-09-957-005-9	Sequence 9, Appl1
40	127	3.8	2099	15 US-10-128-714-3290	Sequence 3290, Ap
41	127	3.8	2405	15 US-10-128-714-8290	Sequence 8290, Ap
42	125.5	3.8	457	9 US-09-815-242-12670	Sequence 12670, A
43	123	3.7	810	12 US-09-769-744A-74	Sequence 74, Appl1
44	122.5	3.7	862	15 US-10-177-293-391	Sequence 391, App
45	122	3.6	46	12 US-10-029-386-30160	Sequence 30160, A

## ALIGNMENTS

RESULT 1

US-10-080-370-6

Sequence 6, Application US/10080370

Publication No. US20030166532A1

GENERAL INFORMATION:

APPLICANT: Allison, Anthony

TITLE OF INVENTION: Modified Annexin Proteins and Methods for Preventing Thrombosis

FILE REFERENCE: SUPP.30

CURRENT APPLICATION NUMBER: US/10/080.370

PRIOR FILING DATE: 2002-02-21

PRIOR APPLICATION NUMBER: 60/270.402

PRIOR FILING DATE: 2001-02-21

PRIOR APPLICATION NUMBER: 60/332.582

NUMBER OF SEQ ID NOS: 9

SOFTWARE: PatentIn version 3.1

SEQ ID NO 6

LENGTH: 669

TYPE: PRT

ORGANISM: Artificial sequence

FEATURE:

NAME/KEY: misc.feature

LOCATION: (15)..(15)

OTHER INFORMATION: The 'Xaa' at location 15 stands for Ser.

NAME/KEY: misc.feature

LOCATION: (334)..(334)

OTHER INFORMATION: The 'Xaa' at location 334 stands for Lys, Asn, Arg, Ser, Thr.

OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop cod

NAME/KEY: misc.feature

LOCATION: (351)..(351)

OTHER INFORMATION: The 'Xaa' at location 351 stands for Lys, Asn, Arg, Ser, Thr.

OTHER INFORMATION: Met, Glu, Asp, Gly, Ala, Val, Gln, His, Pro, Leu, a stop cod

NAME/KEY: misc.feature

LOCATION: (45)..(45)

OTHER INFORMATION: n = a, c, g, or t

NAME/KEY: misc.feature  
 LOCATION: (1000)..(1002)  
 OTHER INFORMATION: n = a, c, g, or t  
 NAME/KEY: misc.feature  
 LOCATION: (1051)..(1053)  
 OTHER INFORMATION: n = a, c, g, or t  
 US-10-080-370-6

Query Match 99.8%; Score 3337; DB 12; Length 669;  
 Best Local Similarity 100.0%; Pred. No. 2,9e-269;  
 Matches 669; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDYKDDDKLAANYALRGVITDTSFGDGRADAEVLRKANKGLGTDEDSILNLTARSA 60  
 DB 1 MDYKDDDKLAANYALRGVITDTSFGDGRADAEVLRKANKGLGTDEDSILNLTARSA 60  
 QY 61 OROQIAEEFKTLFGSDLVNDKSELTKFEKLIYALMKPSRLYDAVELKAKUGAGTDEK 120  
 DB 61 OROQIAEEFKTLFGSDLVNDKSELTKFEKLIYALMKPSRLYDAVELKAKUGAGTDEK 120  
 QY 121 VLTEIIASRTPEELRAIKQAYEEYGSNLEDDVVGDTSGYQRMVLLQANRDPDTAID 180  
 DB 121 VLTEIIASRTPEELRAIKQAYEEYGSNLEDDVVGDTSGYQRMVLLQANRDPDTAID 180  
 QY 181 DAQVELDAQALFQAGELKMGTEDEKFTIIGTSVSHLRVFPKMTTISGFQIEETIDRE 240  
 DB 181 DAQVELDAQALFQAGELKMGTEDEKFTIIGTSVSHLRVFPKMTTISGFQIEETIDRE 240  
 QY 241 TSGNLENLLAVKSIISIPAYLAETLYAMKAGTDDHILIRIYSRSEIDLFINRKEF 300  
 DB 241 TSGNLENLLAVKSIISIPAYLAETLYAMKAGTDDHILIRIYSRSEIDLFINRKEF 300  
 QY 301 RKNFATSIYSMTKIDTSGDYKAKALLCGGEDYKRSRSGLEVFQCGSTXALRGVTDF 360  
 DB 301 RKNFATSIYSMTKIDTSGDYKAKALLCGGEDYKRSRSGLEVFQCGSTXALRGVTDF 360  
 QY 361 SGFDRADAEVLRKANKGLGTDEDSILNLTARSAOQOIAEEFKTLFGSDLVNDKSE 420  
 DB 361 SGFDRADAEVLRKANKGLGTDEDSILNLTARSAOQOIAEEFKTLFGSDLVNDKSE 420  
 QY 421 LTGFEKLIYALMKPSRLYDAVELKAKUGAGTDEKLTETIIASRTPEELRAIKQAYEE 480  
 DB 421 LTGFEKLIYALMKPSRLYDAVELKAKUGAGTDEKLTETIIASRTPEELRAIKQAYEE 480  
 QY 481 YGSNLEDDVVGDTSGYQRMVLLQANRDPDTAIDDAQVELDAQALFQAGELKMGTEDE 540  
 DB 481 YGSNLEDDVVGDTSGYQRMVLLQANRDPDTAIDDAQVELDAQALFQAGELKMGTEDE 540  
 QY 541 KFTIIGTSVSHLRVFPKMTTISGFQIEETIDRETSNLENLLAVKSIISIPAYLA 600  
 DB 541 KFTIIGTSVSHLRVFPKMTTISGFQIEETIDRETSNLENLLAVKSIISIPAYLA 600  
 QY 601 ETLVYAMKAGTDDHILIRIYSRSEIDLFINRKEKRFATSLYSMTKIDTSGDYKAL 660  
 DB 601 ETLVYAMKAGTDDHILIRIYSRSEIDLFINRKEKRFATSLYSMTKIDTSGDYKAL 660  
 QY 661 LLLCGGEDD 669  
 DB 661 LLLCGGEDD 669

RESULT 2  
 US-10-080-370-3  
 Sequence 3, Application US/10080370  
 Publication No. US20030166532A1  
 GENERAL INFORMATION:  
 APPLICANT: Allison, Anthony  
 TITLE OF INVENTION: Modified Annexin Proteins and Methods for Preventing Thrombosis  
 FILE REFERENCE: SDR 90  
 CURRENT APPLICATION NUMBER: US/10/080,370  
 CURRENT FILING DATE: 2002-02-21  
 PRIOR APPLICATION NUMBER: 60/270,402  
 PRIOR FILING DATE: 2001-02-21

PRIOR APPLICATION NUMBER: 60/332,582  
 PRIOR FILING DATE: 2001-11-21  
 NUMBER OF SEQ ID NOS: 9  
 SOFTWARE: PatentIn version 3.1  
 SEQ ID NO 3  
 LENGTH: 319  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-080-370-3

Query Match 47.7%; Score 1593; DB 12; Length 319;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-124;  
 Matches 319; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ALRGVITDTSFGDGRADAEVLRKANKGLGTDEDSILNLTARSAOQOIAEEFKTLFG 75  
 DB 2 ALRGVITDTSFGDGRADAEVLRKANKGLGTDEDSILNLTARSAOQOIAEEFKTLFG 75  
 QY 76 DLVNDKSELTKFEKLIYALMKPSRLYDAVELKAKUGAGTDEKLTETIIASRTPEEL 135  
 DB 76 DLVNDKSELTKFEKLIYALMKPSRLYDAVELKAKUGAGTDEKLTETIIASRTPEEL 135  
 QY 136 AIKQAYEEYGSNLEDDVVGDTSGYQRMVLLQANRDPDTAIDDAQVELDAQALFQAG 195  
 DB 136 AIKQAYEEYGSNLEDDVVGDTSGYQRMVLLQANRDPDTAIDDAQVELDAQALFQAG 195  
 QY 196 ELKMGTEDEKFTIIGTSVSHLRVFPKMTTISGFQIEETIDRETSNLENLLAVKS 255  
 DB 196 ELKMGTEDEKFTIIGTSVSHLRVFPKMTTISGFQIEETIDRETSNLENLLAVKS 255  
 QY 256 IRSIPAYLAETLYAMKAGTDDHILIRIYSRSEIDLFINRKEKRFATSLYSMTKID 315  
 DB 256 IRSIPAYLAETLYAMKAGTDDHILIRIYSRSEIDLFINRKEKRFATSLYSMTKID 315  
 QY 316 TSGDYKAKALLCGGEDD 333  
 DB 302 TSGDYKAKALLCGGEDD 315

RESULT 3  
 US-10-007-761-72  
 Sequence 72, Application US/10007761  
 Publication No. US20020150984A1  
 GENERAL INFORMATION:  
 APPLICANT: Noguchi-Kosen, Darja  
 TITLE OF INVENTION: Peptides for Activation and Inhibition  
 FILE REFERENCE: 58600-8208; US00  
 CURRENT APPLICATION NUMBER: US/10/007,761  
 CURRENT FILING DATE: 2001-11-09  
 PRIOR APPLICATION NUMBER: US 60/262,060  
 PRIOR FILING DATE: 2001-01-18  
 NUMBER OF SEQ ID NOS: 72  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 72  
 LENGTH: 320  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-007-761-72

Query Match 43.4%; Score 1451.5; DB 14; Length 320;  
 Best Local Similarity 91.5%; Pred. No. 2.4e-112;  
 Matches 290; Conservative 12; Mismatches 14; Indels 1; Gaps 1;

QY 17 LRGTVDTSFGDGRADAEVLRKANKGLGTDEDSILNLTARSAOQOIAEEFKTLFG 76  
 DB 5 LRGTVDTSFGDGRADAEVLRKANKGLGTDEDSILNLTARSAOQOIAEEFKTLFG 76  
 QY 77 LVDKSELTKFEKLIYALMKPSRLYDAVELKAKUGAGTDEKLTETIIASRTPEELRA 136  
 DB 65 LVDKSELTKFEKLIYALMKPSRLYDAVELKAKUGAGTDEKLTETIIASRTPEELRA 124  
 QY 137 IKQAYEEYGSNLEDDVVGDTSGYQRMVLLQANRDPDTAIDDAQVELDAQALFQAG 196

Db 125 IKQVYEEYGSLEDDVVGDTSGYQRMVLVLLQANRPDPAIDAEQVBDQAALFQAGE 184  
QY 197 LKMGTDDEKFTITLIGTSVSHLRVFDKXMTISGFOIETTIDRETSQNLLELLAVVXS1 256  
Db 185 LKMGTDDEKFTITIGTSVSHLRKVFDPKXMTISGFOIETTIDRETSQNLLELLAVVXS1 244  
QY 257 RSIPAYLAETLYAAKAGAGTDHDLIRIVSRSEIDLFINIKERKXKPAISLVMIGDT 316  
Db 245 RSIPAYLAETLYAAKAGAGTDHDLIRVWVSRSSEIDLFINIKERKXKPAISLVMIGDT 304  
QY 317 SGDYKXKALLLCCGEDD 333  
Db 305 SGDYKXKALLLCCGEDD 320

RESULT 4  
US-09-970-969-2

/ Sequence 2, Application US/09970969  
/ Patent No. US20020103341A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Tait, Jonathan F.  
/ TITLE OF INVENTION: Annexin Derivatives with Endogenous Chelation Sites  
/ FILE REFERENCE: uotw-1-13841  
/ CURRENT APPLICATION NUMBER: US/09/970,969  
/ CURRENT FILING DATE: 2001-10-03  
/ NUMBER OF SEQ ID NOS: 6  
/ SOFTWARE: PatentIn Ver. 2.0  
/ SEQ ID NO 2  
/ LENGTH: 327  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
US-09-970-969-2

Query Match 43.1%; Score 1442.5; DB 10; Length 327;  
Best Local Similarity 91.2%; Pred. No. 1.4e-111;  
Matches 289; Conservative 12; Mismatches 15; Indels 1; Gaps 1;

QY 17 LRGTVTFSGFDGADAEVLRKAMKGLGTDDESIINLITARSNAQOQIAEEFKTLFGRD 76  
Db 12 LRGTVTFSGFDGADAEVLRKAMKGLGTDDESIINLITARSNAQOQISAAFKTLFGRD 71  
QY 77 LNDMKSLELTGKFEKLIYALMKPSRLYDAYELKHAUKAGAGTDEKVLTEIIASRTPEELRA 136  
Db 72 LDDDKSELTLGKFEKLIYALMKPSRLYDAYELKHAUKAGAGTDEKVLTEIIASRTPEELRA 131  
QY 137 IKQAYEEYGSNLEDDVVGDTSGYQRMVLVLLQANRPDPAIDAEQVBDQAALFQAGE 196  
Db 132 IKQAYEEYGSNLEDDVVGDTSGYQRMVLVLLQANRPDPAIDAEQVBDQAALFQAGE 191  
QY 197 LKMGTDDEKFTITLIGTSVSHLRVFDKXMTISGFOIETTIDRETSQNLLELLAVVXS1 256  
Db 192 LKMGTDDEKFTITIGTSVSHLRKVFDPKXMTISGFOIETTIDRETSQNLLELLAVVXS1 251  
QY 257 RSIPAYLAETLYAAKAGAGTDHDLIRIVSRSEIDLFINIKERKXKPAISLVMIGDT 316  
Db 252 RSIPAYLAETLYAAKAGAGTDHDLIRVWVSRSSEIDLFINIKERKXKPAISLVMIGDT 311  
QY 317 SGDYKXKALLLCCGEDD 333  
Db 312 SGDYKXKALLLCCGEDD 327

RESULT 5  
US-09-970-969-4  
/ Sequence 4, Application US/09970969  
/ Patent No. US20020103341A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Tait, Jonathan F.  
/ APPLICANT: Brown, David S.  
/ TITLE OF INVENTION: Annexin Derivatives with Endogenous Chelation Sites  
/ FILE REFERENCE: uotw-1-13841

/ CURRENT APPLICATION NUMBER: US/09/970,969  
/ CURRENT FILING DATE: 2001-10-03  
/ NUMBER OF SEQ ID NOS: 6  
/ SOFTWARE: PatentIn Ver. 2.0  
/ SEQ ID NO 4  
/ LENGTH: 327  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
US-09-970-969-4

Query Match 43.1%; Score 1442.5; DB 10; Length 327;  
Best Local Similarity 91.2%; Pred. No. 1.4e-111;  
Matches 289; Conservative 12; Mismatches 15; Indels 1; Gaps 1;

QY 17 LRGTVTFSGFDGADAEVLRKAMKGLGTDDESIINLITARSNAQOQIAEEFKTLFGRD 76  
Db 12 LRGTVTFSGFDGADAEVLRKAMKGLGTDDESIINLITARSNAQOQISAAFKTLFGRD 71  
QY 77 LNDMKSLELTGKFEKLIYALMKPSRLYDAYELKHAUKAGAGTDEKVLTEIIASRTPEELRA 136  
Db 72 LDDDKSELTLGKFEKLIYALMKPSRLYDAYELKHAUKAGAGTDEKVLTEIIASRTPEELRA 131  
QY 137 IKQAYEEYGSNLEDDVVGDTSGYQRMVLVLLQANRPDPAIDAEQVBDQAALFQAGE 196  
Db 132 IKQAYEEYGSNLEDDVVGDTSGYQRMVLVLLQANRPDPAIDAEQVBDQAALFQAGE 191  
QY 197 LKMGTDDEKFTITIGTSVSHLRVFDKXMTISGFOIETTIDRETSQNLLELLAVVXS1 256  
Db 192 LKMGTDDEKFTITIGTSVSHLRKVFDPKXMTISGFOIETTIDRETSQNLLELLAVVXS1 251  
QY 257 RSIPAYLAETLYAAKAGAGTDHDLIRIVSRSEIDLFINIKERKXKPAISLVMIGDT 316  
Db 252 RSIPAYLAETLYAAKAGAGTDHDLIRVWVSRSSEIDLFINIKERKXKPAISLVMIGDT 311  
QY 317 SGDYKXKALLLCCGEDD 333  
Db 312 SGDYKXKALLLCCGEDD 327

RESULT 6  
US-09-970-969-6  
/ Sequence 6, Application US/09970969  
/ Patent No. US20020103341A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Tait, Jonathan F.  
/ APPLICANT: Brown, David S.  
/ TITLE OF INVENTION: Annexin Derivatives with Endogenous Chelation Sites  
/ FILE REFERENCE: uotw-1-13841  
/ CURRENT APPLICATION NUMBER: US/09/970,969  
/ CURRENT FILING DATE: 2001-10-03  
/ NUMBER OF SEQ ID NOS: 6  
/ SOFTWARE: PatentIn Ver. 2.0  
/ SEQ ID NO 6  
/ LENGTH: 327  
/ TYPE: PRT  
/ ORGANISM: Homo sapiens  
US-09-970-969-6

Query Match 43.1%; Score 1442.5; DB 10; Length 327;  
Best Local Similarity 91.2%; Pred. No. 1.4e-111;  
Matches 289; Conservative 12; Mismatches 15; Indels 1; Gaps 1;

QY 17 LRGTVTFSGFDGADAEVLRKAMKGLGTDDESIINLITARSNAQOQIAEEFKTLFGRD 76  
Db 12 LRGTVTFSGFDGADAEVLRKAMKGLGTDDESIINLITARSNAQOQISAAFKTLFGRD 71  
QY 77 LNDMKSLELTGKFEKLIYALMKPSRLYDAYELKHAUKAGAGTDEKVLTEIIASRTPEELRA 136  
Db 72 LDDDKSELTLGKFEKLIYALMKPSRLYDAYELKHAUKAGAGTDEKVLTEIIASRTPEELRA 131  
QY 137 IKQAYEEYGSNLEDDVVGDTSGYQRMVLVLLQANRPDPAIDAEQVBDQAALFQAGE 196  
Db 132 IKQAYEEYGSNLEDDVVGDTSGYQRMVLVLLQANRPDPAIDAEQVBDQAALFQAGE 191

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QY 197 LKMGDEEKFITLIGTSVSHLRVDPKXMTISGFOJETIDRETSNGNLENTLLAVVSI 256
DB 192 LKMGDEEKFITLIGTSVSHLRVDPKXMTISGFOJETIDRETSNGNLENTLLAVVSI 251
QY 257 RSPAYLAETLYYAMKAGAGTDDHTLIRVYSRSEIDLFINRKEFRKNFATSYSMTKQDT 316
DB 252 RSPAYLAETLYYAMKAGAGTDDHTLIRVYSRSEIDLFINRKEFRKNFATSYSMTKQDT 311
QY 317 SGDYKXALLLGGEDD 333
DB 312 SGDYKXALLLGGEDD 327

RESULT 7
US-10-097-340-10
; Sequence 10, Application US/10097340
; Publication No. US200306087250A1
; GENERAL INFORMATION:
; APPLICANT: John MOWHAN
; APPLICANT: Manjula GANNANARAPU
; APPLICANT: Sebastian HOERSCH
; APPLICANT: Shubhangl KAMATKAR
; APPLICANT: Steve G KOVATS
; APPLICANT: Rachel E. MEYERS
; APPLICANT: Michael MORRISSEY
; APPLICANT: Peter OLANDT
; APPLICANT: Ami SEN
; APPLICANT: Peter VEIBY
; APPLICANT: Gordon B. MILLS
; APPLICANT: Robert C. BAST, Jr.
; APPLICANT: Rosemarie SCHMANDT
; APPLICANT: Xumei ZHAO
; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins for The Identification,
; TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
; FILE REFERENCE: MRI-030
; CURRENT APPLICATION NUMBER: US/10/097,340
; PRIOR FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: 60/276,025
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/325,149
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/276,026
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/324,967
; PRIOR FILING DATE: 2001/09/26
; PRIOR APPLICATION NUMBER: 60/311,732
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/325,102
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/323,580
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 321
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-097-340-10

Query Match 27.6%; Score 921; DB 15; Length 321;
Best Local Similarity 57.3%; Pred. No. 2.4e-68;
Matches 180; Conservative 56; Mismatches 78; Indels 0; Gaps 0;
QY 19 GTVDFSGFDGRADAEVLKRAKMGIGTDEDSINLITRASNAGQOIAEEFKTLFGRLDV 78
DB 8 GTVAAASGFNAMEDAQTLRKAMKGLGTDEDAIISVLAYRNTAOROEIRTAVKSTIGRDLI 67
QY 79 NDMKSELTGKFEKTLIVLAKMSPRLYDAVELKHAHLGAGTDEKVLTEIIASRTPEELRAIK 138
DB 68 DNVASELSGNFEQYIVGMPTPTVLYDVQVELRARMKAGAGTDEGLIILASRTPEELRIS 127

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QY 139 QAYEEYGSNLEDDVVGDTSGYVORMVLVLQANDPPTAIDDAQVELDAQALFOAGELK 198
DB 128 QTYQQOIGSLBEDLIDSDTSFMFORVLSLSAGGBDESNYDDALVRDADDLVEAGBKK 187
QY 199 WGTDEEKFITLIGTSVSHLRVDPKXMTISGFOJETIDRETSNGNLENTLLAVVSI 258
DB 188 WGTDEKFLTVLCSNRNHLHVPEYKRISQKDIQSKETSGSFEDALLAVKCMRN 247
QY 259 IPAYLAETLYYAMKAGAGTDDHTLIRVYSRSEIDLFINRKEFRKNFATSYSMTKQDTSG 318
DB 248 KSAVFAEKLYKSNKMGIGTDDNTLIRVWVSRAEIDMLDIRAFKRLYKSLYSFIKQDTSG 307
QY 319 DYKXALLLGGEDD 332
DB 308 DYKXALLLGGEDD 321

RESULT 8
US-09-925-301-1062
; Sequence 1062, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1062
; LENGTH: 324
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-301-1062

Query Match 27.6%; Score 921; DB 9; Length 324;
Best Local Similarity 57.3%; Pred. No. 2.5e-68;
Matches 180; Conservative 56; Mismatches 78; Indels 0; Gaps 0;
QY 19 GTVDFSGFDGRADAEVLKRAKMGIGTDEDSINLITRASNAGQOIAEEFKTLFGRLDV 78
DB 11 GTVAAASGFNAMEDAQTLRKAMKGLGTDEDAIISVLAYRNTAOROEIRTAVKSTIGRDLI 70
QY 79 NDMKSELTGKFEKTLIVLAKMSPRLYDAVELKHAHLGAGTDEKVLTEIIASRTPEELRAIK 138
DB 71 DDLKSELGNFEQYIVGMPTPTVLYDVQVELRARMKAGAGTDEGLIILASRTPEELRIS 130
QY 139 QAYEEYGSNLEDDVVGDTSGYVORMVLVLQANDPPTAIDDAQVELDAQALFOAGELK 198
DB 131 QTYQQOIGSLBEDLIDSDTSFMFORVLSLSAGGBDESNYDDALVRDADDLVEAGBKK 190
QY 199 WGTDEEKFITLIGTSVSHLRVDPKXMTISGFOJETIDRETSNGNLENTLLAVVSI 258
DB 191 WGTDEKFLTVLCSNRNHLHVPEYKRISQKDIQSKETSGSFEDALLAVKCMRN 250
QY 259 IPAYLAETLYYAMKAGAGTDDHTLIRVYSRSEIDLFINRKEFRKNFATSYSMTKQDTSG 318
DB 251 KSAVFAEKLYKSNKMGIGTDDNTLIRVWVSRAEIDMLDIRAFKRLYKSLYSFIKQDTSG 310
QY 319 DYKXALLLGGEDD 332
DB 311 DYKXALLLGGEDD 324

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GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
FILE REFERENCE: PA104  
CURRENT APPLICATION NUMBER: US/09/925,302  
CURRENT FILING DATE: 2001-08-10  
PRIOR APPLICATION NUMBER: PCT/US00/05918  
PRIOR FILING DATE: 2000-03-08  
PRIOR APPLICATION NUMBER: 60/124,270  
PRIOR FILING DATE: 1999-03-12  
NUMBER OF SEQ ID NOS: 896  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO: 731  
LENGTH: 208  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-925-302-731

Query Match 26.5%; Score 887; DB 9; Length 208;  
Best Local Similarity 85.9%; Pred. No. 8,6e-66;  
Matches 177; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

QY 10 LAAANXALRGTVDFSGFGRADAETLRKAMKGLGTDEDSILNLTARSMARQCIAEF 69  
DB 1 VVAAQVLRGTVDTPGFGRADAETLRKAMKGLGTDEDSILNLTARSMARQCIASAF 60  
QY 70 KTLFGRDLVNDKSELTGKFEKLIYALMKPSRLYDAYELKHAKEAGTDEKVTLEIIASR 129  
DB 61 KTLFGRDLVNDKSELTGKFEKLIYALMKPSRLYDAYELKHAKEAGTDEKVTLEIIASR 120  
QY 130 TPEELRAIKQAYEEBEGSNIEDDVADTSGYYQRMVLVLLQANRDPDAIDDAQVELDAQ 189  
DB 121 TPEELRAIKQAYEEBEGSNIEDDVADTSGYYQRMVLVLLQANRDPDAIDDAQVELDAQ 180  
QY 190 ALFOAGELKMGTDSEKFTILGTRSV 215  
DB 181 ALFOAGELKMGTDSEKFTILGTRSV 206

RESULT 10  
US-10-236-031B-18  
Sequence 18; Application US/10236031B  
Publication No. US20030219760A1  
GENERAL INFORMATION:  
APPLICANT: Gordon, Gavin J.  
APPLICANT: Jensen, Roderick V.  
APPLICANT: Gullans, Steven R.  
APPLICANT: Bueno, Raphael  
TITLE OF INVENTION: Diagnostic and Prognostic Tests  
FILE REFERENCE: B00801/70265 (GRV/JAV)  
CURRENT APPLICATION NUMBER: US/10/236, 031B  
CURRENT FILING DATE: 2002-09-05  
PRIOR APPLICATION NUMBER: US 60/317,389  
PRIOR FILING DATE: 2001-09-05  
PRIOR APPLICATION NUMBER: US 60/407,431  
PRIOR FILING DATE: 2002-08-30  
NUMBER OF SEQ ID NOS: 102  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO: 18  
LENGTH: 327  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-236-031B-18

Query Match 24.6%; Score 822.5; DB 12; Length 327;  
Best Local Similarity 56.9%; Pred. No. 3.7e-60;  
Matches 178; Conservative 44; Mismatches 90; Indels 1; Gaps 1;

QY 20 TVNDFSGFGRADAETLRKAMKGLGTDEDSILNLTARSMARQCIAEF 79  
DB 14 TVNDFSGFGRADAETLRKAMKGLGTDEDSILNLTARSMARQCIAEF 73  
QY 80 DMKSELTGKFEKLIYALMKPSRLYDAYELKHAKEAGTDEKVTLEIIASRTPEELRAIKQ 139

DB 74 TLKSELGFEELIYALMKPSRLYDAYELKHAKEAGTDEKVTLEIIASRTPEELRAIKQ 133  
QY 140 AYEESGNSLDEVDVGTSGYYQRMVLVLLQANRDP-DIAIDDAQVELDAQALFOAGELK 198  
DB 134 AYEEDGSSLEBDIQADTSGYLERITVCLLQGRDVSFPDPAALQDADVAAQGBKI 193  
QY 199 WGTDEKFTITIGTSVSHLRVPKMTTIGFQLEETIDRETSQNLNLLAVYSIRS 256  
DB 194 RGTDEKFTITIGTSVSHLRVPKMTTIGFQLEETIDRETSQNLNLLAVYSIRS 253  
QY 259 IPAYLAETLYYAMKAGTDDHTLRVYSRSEIDLFINRKEFRKNFATSLYMKDPTSG 316  
DB 254 LHSYFAERLYYAMKAGTDDHTLRVYSRSEIDLFINRKEFRKNFATSLYMKDPTSG 313  
QY 319 DYKALLILCGGE 331  
DB 314 DYKALLILVGS 326

RESULT 11  
US-10-316-253-262  
Sequence 262; Application US/10316253  
Publication No. US20030162706A1  
GENERAL INFORMATION:  
APPLICANT: The Procter & Gamble Company  
APPLICANT: Peters, Kevin  
APPLICANT: Thompson, Larry  
APPLICANT: Wang, Feng  
APPLICANT: Greis, Kenneth  
TITLE OF INVENTION: Angiogenesis Modulating Proteins  
FILE REFERENCE: 8865M  
CURRENT APPLICATION NUMBER: US/10/316,253  
CURRENT FILING DATE: 2002-12-10  
PRIOR APPLICATION NUMBER: US 60/355,295  
PRIOR FILING DATE: 2002-02-08  
NUMBER OF SEQ ID NOS: 308  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO: 262  
LENGTH: 324  
TYPE: PRT  
ORGANISM: Rattus norvegicus  
US-10-316-253-262

Query Match 23.6%; Score 790; DB 12; Length 324;  
Best Local Similarity 47.9%; Pred. No. 1.8e-57;  
Matches 156; Conservative 65; Mismatches 99; Indels 6; Gaps 1;

QY 343 LFGGPGSTYALRGTVDFSGFGRADAETLRKAMKGLGTDEDSILNLTARSMARQCI 402  
DB 5 LNWGP-----RGITNNYPGPNPSVDAEAIKKAIGTDEKVTLEIIASRTPEELRAIKQ 58  
QY 403 EEFKTLFGRDLVNDKSELTGKFEKLIYALMKPSRLYDAYELKHAKEAGTDEKVTLEII 462  
DB 59 KAIQAYEALKADKGLSGHFEHWVALITAYADAKQKSMGKGTDEDTLEII 118  
QY 463 ASRTEPEELRAIKQAYEEBEGSNIEDDVADTSGYYQRMVLVLLQANRDPDAIDDAQVEL 522  
DB 119 TTRTSRQMEKISQAYYATYKKNLDDISSETSGDFRVALTLADGGSDESLKVDHAKK 178  
QY 523 DAQALFOAGELKMGTDSEKFTILGTRSVSHLRVPKMTTIGFQLEETIDRETSQNLN 562  
DB 179 DAQALFOAGELKMGTDSEKFTILGTRSVSHLRVPKMTTIGFQLEETIDRETSQNLN 528  
QY 583 NLLAVYSIRSIIPAYLAETLYYAMKAGTDDHTLRVYSRSEIDLFINRKEFRKNFAT 642  
DB 239 DILLAVVACTRNTPAFLAGRLHQAQKAGTDEFTLNINVSRSIDLDLRREKRYGC 298  
QY 643 SLYSWKDPTSGDYKALLILCGGED 668  
DB 299 SLYSWKDPTSGDYKALLILCGGED 324

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RESULT 12
US-10-205-823-34
; Sequence 34, Application US/10205823
; Publication No. US20030108963A1
GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gorbacheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Monsey, Angela W.
; APPLICANT: Glatz, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/10/205,823
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-205-823-34

Query Match      23.5%; Score 785; DB 15; Length 323;
Best Local Similarity 48.3%; Pred. No. 4,6e-57;
Matches 152; Conservative 68; Mismatches 95; Indels 0; Gaps 0;

QY 18 RGTVDPSGDFGRADAEVLRKMKGLGTDEDSINLTLAGSNARQOIAEEFKTLRPRDL 77
DB 9 RGTVDPSGDFGRADAEVLRKMKGLGTDEDSINLTLAGSNARQOIAEEFKTLRPRDL 77
78 VDMKSELTGKFEKLIYALMKPSRLYDAYEELKHAQAGTDEKVLTEIIASRTPEELRAI 137
DB 69 KDDLKGLDSGFHEHLMVALVPPPAVFAKQKKSMKAGTVEALTEIILTRTSRQVKDI 128
QY 138 KQAYEEYGSNLEDVVGDDTSGYQRMVLVLCANRPDPTAIDAOVELDAQALFOAGEL 197
DB 129 SQAYTVTKKSLGDISSETSGDFKALLTLADGRRESLKVDDHLAKQDAQILYKAGEN 198
QY 198 KMGTEDEKEITILIGTSVSHLRVVDKMTISGFOIETTIDRTSGNLEMLLAVYSIR 257
DB 189 RMGTDEBKTEILCRSSFPQKLTDEVRNLSQDIYDSINGELSGHFDLLAIYNCAR 248
QY 258 STPAYLAETLYAMKAGTDDHTLRVIVSRSEIDLFINRKEFKAFATLYSMIKGDS 317
DB 249 NTPAFIAERLHRLAKIGIDDEFTLNRIWVSSEIDLDIRTEFKHGYSLYSAIKSDIS 308
QY 318 GDYKALLLLCGGED 332
DB 309 GDYEITILKICGGDD 323

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GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben,
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1664
; LENGTH: 485
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-300-1664

Query Match      22.8%; Score 763.5; DB 10; Length 485;
Best Local Similarity 45.6%; Pred. No. 5e-55;
Matches 154; Conservative 69; Mismatches 114; Indels 1; Gaps 1;

QY 329 CGEDDXSRSGLEVLFGPGPS-IXALRGVTTDFSGDGRADAEVLRKMKGLGTDEDSL 387
DB 147 GGQMPSCYPGGQPTYPSPQPAVTQVGTIRPANPDARDAEILRKMKGGTDEQATV 206
QY 388 NLTARSNARQOIAEEFKTLFGRDLVDMKSELTGKFEKLIYALMKPSRLYDAYEELKHA 447
DB 207 DVANRNDQQRQKIKAFKTSYKDLIKDKSLSSNMELLIALFMPPTYDANSLRA 266
QY 448 KLGAGTDEKVLTEIIASRTPEELRAIKQAYEEYGSNLEDVVGDDTSGYQRMVLVLLQA 507
DB 267 MCGAGTQERVLIELICTRTQCEIRIVRCYQSEFGHDLKDIRSDTSGHFERLLVSMCG 326
QY 508 NRDPPTAIDAOVELDAQALFOAGELKMGTEDEKFTIIGTSVSHLRVFPKMTISGF 567
DB 327 NRDNQSLNMQAEDQRLYQNGEGLGTDESCFMILLATISFPOLRAITWATYSRMNR 386
QY 568 QIEETIDRTSGNLEMLLAVYSIRSPAYLAETLYAMKAGTDDHTLIRIVSRSEI 627
DB 387 DLSVSRERFSGYVESGLKTIILQCALNRPFAERLYAMKAGTDDSTLVIRVTRSEI 446
QY 628 DLFNIRKEFRKNFATLSYMIKGTSGDYKALLLLCG 665
DB 447 DLVOIKQFAMQTKITLGTWAGTSGDYRRLMLAIVG 484

RESULT 14
US-09-974-298-91
; Sequence 91, Application US/09974298
; Publication No. US20020156263A1
GENERAL INFORMATION:
; APPLICANT: Chen, Hwei-Mei,
; TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER
; FILE REFERENCE: PA-0037 P
; CURRENT APPLICATION NUMBER: US/09/974,298
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/236,331
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PERL Program
; SEQ ID NO 91
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: incyte ID No. US20020156263A1 1378745CD1
US-09-974-298-91

Query Match      20.8%; Score 695.5; DB 10; Length 339;
Best Local Similarity 45.4%; Pred. No. 1.3e-49;

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Matches 143; Conservative 67; Mismatches 104; Indels 1; Gaps 1;

QY 19 GTYDFSGFDGRDAEVLKRAKMGGLTDEDSILNLTARSAQROQIAEERKTLFGRLV 78  
 Db 25 GSVAYATNFDAERDANIETAIKTKGVDEVITVILNRSNAQRODIAFAVORRTKKELA 84  
 QY 79 NDMKSELTKGFEKFLIVALKMPSRLYDAYELGAHKGAGTDEKVLTEIIASRTPEELPAIK 138  
 Db 85 SALKSALSGHLETVILGLKTPAQYDASELSKMGGLTDEDSLIEIICSRNQELOEIN 144  
 QY 139 QAVEEYGSNLEDDVVGDTSGYYQRLVLLQANRDPD-TAIDDAQVELDAQALFOAGEL 197  
 Db 145 RYKEMKYTDLEKDIISDTSGDFRKLMAKGRRAEDGSVIDYELIDQDARDLYDAGVK 204  
 QY 198 KMGTEDEKFTITLIGTSVSHLRVFDKMTISGFOIETITDRETSGNLEMLLAIVKSR 257  
 Db 205 RKGTDVPMKWSITERSVPHLQKQVDRYKSYSPYDLESIRKEVYGDLENFNLVQCIO 264  
 QY 258 SIPAYLAETLYYAMKAGTDDHTLIRIVSRSEIDLFINRKEFRKFNATSLYSXIKGDTG 317  
 Db 265 NKPLVFADRLYDSMKGKTGRDKVLIRIMVSRSEVDMKIRSEFRKXKGLYYTIQDDTK 324  
 QY 318 GDYKALLILCGED 332  
 Db 325 GDYQKALLYLGGDD 339

## RESULT 15

US-10-097-340-6

Sequence 6, Application US/10097340

Publication No. US2003087250A1

GENERAL INFORMATION:

APPLICANT: John MONAHAN  
 APPLICANT: Manjula GANNAVAPU  
 APPLICANT: Sebastian HOERSCHE  
 APPLICANT: Shubhangi KAMATKAR  
 APPLICANT: Steve G. KOVATIS  
 APPLICANT: Rachel E. MEYERS  
 APPLICANT: Michael MORRISSEY  
 APPLICANT: Peter OLANDT  
 APPLICANT: Aml SEN  
 APPLICANT: Peter VERIBY  
 APPLICANT: Gordon B. MILLS  
 APPLICANT: Robert C. BAST, Jr.  
 APPLICANT: Karen LY  
 APPLICANT: Rosemarie SCHMANDT  
 APPLICANT: Xumei ZHAO  
 APPLICANT: Karen GLATT  
 TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,  
 FILE REFERENCE: Assessment, Prevention, and Therapy of Ovarian Cancer  
 FILE REFERENCE: NRI-030  
 CURRENT APPLICATION NUMBER: US/10/097,340  
 CURRENT FILING DATE: 2002-03-14  
 PRIOR APPLICATION NUMBER: 60/276,025  
 PRIOR FILING DATE: 2001-03-14  
 PRIOR APPLICATION NUMBER: 60/325,149  
 PRIOR FILING DATE: 2001-09-26  
 PRIOR APPLICATION NUMBER: 60/276,026  
 PRIOR FILING DATE: 2001-03-14  
 PRIOR APPLICATION NUMBER: 60/324,967  
 PRIOR FILING DATE: 2001/09/26  
 PRIOR APPLICATION NUMBER: 60/311,732  
 PRIOR FILING DATE: 2001-09-10  
 PRIOR APPLICATION NUMBER: 60/325,102  
 PRIOR FILING DATE: 2001-09-26  
 PRIOR APPLICATION NUMBER: 60/323,580  
 PRIOR FILING DATE: 2001-09-19  
 NUMBER OF SEQ ID NOS: 363  
 SOFTWARE: FastSeq for Windows Version 4.0  
 SEQ ID NO 6  
 LENGTH: 339  
 TYPE: PRT  
 ORGANISM: Homo sapiens

US-10-097-340-6

Query Match 20.8%; Score 695.5; DB 15; Length 339;

Best Local Similarity 45.4%; Pred. No. 1,36-49;

Matches 143; Conservative 67; Mismatches 104; Indels 1; Gaps 1;

QY 19 GTYDFSGFDGRDAEVLKRAKMGGLTDEDSILNLTARSAQROQIAEERKTLFGRLV 78  
 Db 25 GSVAYATNFDAERDANIETAIKTKGVDEVITVILNRSNAQRODIAFAVORRTKKELA 84  
 QY 79 NDMKSELTKGFEKFLIVALKMPSRLYDAYELGAHKGAGTDEKVLTEIIASRTPEELPAIK 138  
 Db 85 SALKSALSGHLETVILGLKTPAQYDASELSKMGGLTDEDSLIEIICSRNQELOEIN 144  
 QY 139 QAVEEYGSNLEDDVVGDTSGYYQRLVLLQANRDPD-TAIDDAQVELDAQALFOAGEL 197  
 Db 145 RYKEMKYTDLEKDIISDTSGDFRKLMAKGRRAEDGSVIDYELIDQDARDLYDAGVK 204  
 QY 198 KMGTEDEKFTITLIGTSVSHLRVFDKMTISGFOIETITDRETSGNLEMLLAIVKSR 257  
 Db 205 RKGTDVPMKWSITERSVPHLQKQVDRYKSYSPYDLESIRKEVYGDLENFNLVQCIO 264  
 QY 258 SIPAYLAETLYYAMKAGTDDHTLIRIVSRSEIDLFINRKEFRKFNATSLYSXIKGDTG 317  
 Db 265 NKPLVFADRLYDSMKGKTGRDKVLIRIMVSRSEVDMKIRSEFRKXKGLYYTIQDDTK 324  
 QY 318 GDYKALLILCGED 332  
 Db 325 GDYQKALLYLGGDD 339

Search completed: December 12, 2003, 14:54:31  
 Job time : 37.2419 secs



GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: December 12, 2003, 14:43:27 ; Search time 24.613 Seconds  
(without alignments)  
2036.647 Million cell updates/sec

Title: PCT-US03-24332-3

Perfect score: 1598  
Sequence: 1 MALRGVTVPFGSDGRADAE.....GDTSGDYKALLLCGGEHD 319

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Listing first 45 summaries

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24: /SIDSI/gcgdata/Geneseq/genesqp-emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1598	100.0	319	24	ABP56248 Human annexin V pr
2	1593	99.7	659	24	ABP56249 Modified annexin p
3	1580	98.9	318	20	AA113925 65ST GFP variant/h
4	1575	98.6	319	16	AA875695 Rat annexin-V. Ra
5	1535	96.1	319	20	AA113924 65ST GFP variant/h
6	1535	96.1	319	23	AB857067 Mouse ischaemic co
7	1451.5	90.8	319	13	AA846276 CPB-1. Homo sapie
8	1451.5	90.8	319	14	AA841021 Calphobindin I (CP
9	1451.5	90.8	319	23	ABG32550 Human CPB-1 protei

10	1451.5	90.8	320	9	AA880511 Placental coagulat
11	1451.5	90.8	320	10	AA891953 Vascular anti-coag
12	1451.5	90.8	320	12	AA813082 PAP-I. Homo sapie
13	1451.5	90.8	320	20	AA131923 65ST GFP variant/h
14	1451.5	90.8	320	21	AA84788 Amino acid sequenc
15	1451.5	90.8	320	23	ABG31220 Human annexin V, c
16	1448.5	90.6	320	21	AA890053 anti-coagulant Pp4
17	1448.5	90.6	320	21	AA892930 Annexin V/uorokins
18	1447.5	90.6	320	9	AA892317 PAP-I isolated fro
19	1446.5	90.5	319	13	AA826180 CPB-1. Homo sapie
20	1445.5	90.5	320	9	AA880242 Sequence vascular
21	1445.5	90.5	320	9	AA880714 Sequence vascular
22	1445.5	90.5	320	12	AA811910 Vascular anticoagu
23	1442.5	90.3	327	22	AA850863 Modified human ann
24	1442.5	90.3	327	22	AA850864 Modified human ann
25	1442.5	90.3	327	22	AA850865 Modified human ann
26	1441.5	90.2	320	10	AA891363 Human lipocortin-V
27	1419.5	88.8	319	13	AA825718 CPB-1. Homo sapie
28	921	57.6	321	20	AA131926 65ST GFP variant/h
29	921	57.6	321	23	ABG96279 Human ovarian cano
30	921	57.6	324	21	AA84617 Human cancer assoc
31	920	57.6	321	10	AA891913 Anticoagulative pp
32	920	57.6	786	11	AA803726 Human placenta-der
33	919	57.5	672	11	AA803725 Human placenta-der
34	919	57.5	675	24	ABU54621 Human NOVX polypep
35	904.5	56.6	320	21	AA84790 Amino acid sequenc
36	886	55.4	208	21	AA856393 Lung cancer associ
37	870	54.4	503	14	AA834127 Annexin XI type I
38	862	53.9	505	14	AA834128 Annexin XI type I
39	858	53.7	505	20	AA807117 Lung cancer associ
40	852	53.3	299	23	ABP6394 Human polypeptide
41	850	51.2	736	22	ABG19948 Novel human diagno
42	822.5	51.5	327	9	AA880715 Sequence vascular
43	822.5	51.5	327	10	AA891954 Vascular anti-coag
44	822.5	51.5	327	14	AA835754 VAC-beta. Synthet
45	822.5	51.5	327	22	AA878665 Human protein SEQ

#### ALIGNMENTS

RESULT 1  
ABP56248  
ID ABP56248 standard; Protein; 319 AA.  
XX  
AC ABP56248;  
XX  
DT 28-MAR-2003 (first entry)  
XX  
XX Human annexin V protein SEQ ID NO:3.  
DE  
XX  
XX Annexin; modified; thrombosis; annexin V; thrombolytic;  
KW coronary thrombosis; overt cerebral thrombosis; arterial  
KW transient cerebral ischaemic attack; venous thrombosis.  
XX  
OS Homo sapiens.  
XX  
XX WO200267857-A2.  
XX  
XX  
PD 06-SEP-2002.  
XX  
PF 21-FEB-2002; 2002WO-US05079.  
XX  
XX  
PR 21-FEB-2001; 2001US-270402P.  
XX  
PR 21-NOV-2001; 2001US-332582P.  
PA  
XX (SURR-) SURROMED INC.  
XX  
PI Allison A;  
XX  
XX WPI; 2003-129062/12.  
DR N-PSDB; AB221925.  
XX  
XX

PT Novel isolated modified annexin proteins comprising annexin protein  
 PT coupled to polyethylene glycol or additional proteins, useful for  
 PT treating thrombosis e.g. coronary thrombosis and overt cerebral  
 PT thrombosis -  
 XX  
 XX  
 PS Claim 6, Page 36, 62pp; English.  
 CC The present invention describes a modified annexin protein (I) comprising  
 CC an annexin protein coupled to: (i) polyethylene glycol (PEG); or (ii) an  
 CC additional protein. (I) has thrombolytic activity and can be used as a  
 CC thrombosis modulator, and an inhibitor of cellular and humoral  
 CC mechanisms by which platelet aggregation is amplified. (I) can be used  
 CC for treating a subject at risk from thrombosis. Preferably, a  
 CC pharmaceutical composition comprising (I) is administered to a subject  
 CC after coronary thrombosis, overt cerebral thrombosis, or transient  
 CC cerebral ischaemic attack. More preferably, the pharmaceutical  
 CC composition is administered to a diabetic patient who is at risk of  
 CC arterial thrombosis. The pharmaceutical composition can also be  
 CC administered during pregnancy or parturition. (I) is also useful for  
 CC treating arterial or venous thrombosis caused by any medical procedure  
 CC or condition as described above. (I) prevents arterial or venous  
 CC thrombosis without increasing haemorrhage. The present sequence  
 CC represents human annexin V, which is used in an example from the  
 CC present invention.  
 CC  
 SQ Sequence 319 AA;  
 Query Match 100.0%; Score 1598; DB 24; Length 319;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-134;  
 Matches 319; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MALRGVTDFSGFGRADAEVLKRAKMGIGTDEDSITLNLTAASNORQOIAEFTPLFG 60  
 DB 1 MALRGVTDFSGFGRADAEVLKRAKMGIGTDEDSITLNLTAASNORQOIAEFTPLFG 60  
 QY 61 RDLVNDKMSSELTGFEKELIVALKMPSRLYDAVELKAKLGAGTDEKYLEIIASRTPEEL 120  
 DB 61 RDLVNDKMSSELTGFEKELIVALKMPSRLYDAVELKAKLGAGTDEKYLEIIASRTPEEL 120  
 QY 121 RAIKQAYEEYGSNLEDVVDGTSGYQRMVLVLLQANRPPDAIDAQVELDAQLFQA 180  
 DB 121 RAIKQAYEEYGSNLEDVVDGTSGYQRMVLVLLQANRPPDAIDAQVELDAQLFQA 180  
 QY 181 GELKMGIDEEKFTITLIGRSVSHLRVFDKMTISGQIETIDRETSGLNELLAAVVK 240  
 DB 181 GELKMGIDEEKFTITLIGRSVSHLRVFDKMTISGQIETIDRETSGLNELLAAVVK 240  
 QY 241 SIRSIPTAYLAEITLYAMKAGAGTDHTLIRIVSSSEIDLFNIRKPKPAISLYSMIMG 300  
 DB 241 SIRSIPTAYLAEITLYAMKAGAGTDHTLIRIVSSSEIDLFNIRKPKPAISLYSMIMG 300  
 QY 301 DTSGDYKKALLLLCGGEDD 319  
 DB 301 DTSGDYKKALLLLCGGEDD 319  
 RESULT 2  
 ABP56249  
 ID ABP56249 standard; Protein; 669 AA.  
 XX  
 XX ABP56249;  
 XX  
 XX 28-MAR-2003 (first entry)  
 DE Modified annexin protein SEQ ID NO:6.  
 XX  
 XX Annexin: modified; thrombosis; annexin V; thrombolytic;  
 XX coronary thrombosis; overt cerebral thrombosis; arterial thrombosis;  
 XX transient cerebral ischaemic attack; venous thrombosis.  
 OS Homo sapiens.  
 OS Synthetic.

FH Key Location/Qualifiers  
 FT Misc-difference 15 /label= unknown  
 FT /note= "encoded by TCN"  
 FT  
 FT Misc-difference 334 /label= unknown  
 FT /note= "encoded by NNN"  
 FT  
 FT Misc-difference 351 /label= unknown  
 FT /note= "encoded by NNN"  
 FN WO200267857-A2.  
 XX  
 XX 06-SEP-2002.  
 PD  
 XX  
 XX 21-FEB-2002; 2002MO-US05079.  
 PF  
 XX  
 XX 21-FEB-2001; 2001US-270402P.  
 PR  
 XX  
 XX 21-NOV-2001; 2001US-332582P.  
 PA (SURR-) SURROMED INC.  
 PI Allison A;  
 XX  
 XX WPI; 2003-129062/12.  
 DR  
 XX  
 XX N-PSDB; AB221926.  
 DR  
 XX  
 XX  
 PT Novel isolated modified annexin proteins comprising annexin protein  
 PT coupled to polyethylene glycol or additional proteins, useful for  
 PT treating thrombosis e.g. coronary thrombosis and overt cerebral  
 PT thrombosis -  
 XX  
 XX  
 PS Claim 6, Page 59-62; 62pp; English.  
 CC The present invention describes a modified annexin protein (I) comprising  
 CC an annexin protein coupled to: (i) polyethylene glycol (PEG); or (ii) an  
 CC additional protein. (I) has thrombolytic activity and can be used as a  
 CC thrombosis modulator, and an inhibitor of cellular and humoral  
 CC mechanisms by which platelet aggregation is amplified. (I) can be used  
 CC for treating a subject at risk from thrombosis. Preferably, a  
 CC pharmaceutical composition comprising (I) is administered to a subject  
 CC after coronary thrombosis, overt cerebral thrombosis, or transient  
 CC cerebral ischaemic attack. More preferably, the pharmaceutical  
 CC composition is administered to a diabetic patient who is at risk of  
 CC arterial thrombosis. The pharmaceutical composition can also be  
 CC administered during pregnancy or parturition. (I) is also useful for  
 CC treating arterial or venous thrombosis caused by any medical procedure  
 CC or condition as described above. (I) prevents arterial or venous  
 CC thrombosis without increasing haemorrhage. The present sequence  
 CC represents a modified annexin protein from the present invention.  
 CC  
 SQ Sequence 669 AA;  
 Query Match 99.7%; Score 1593; DB 24; Length 669;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-133;  
 Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 ALRGVTDFSGFGRADAEVLKRAKMGIGTDEDSITLNLTAASNORQOIAEFTPLFG 61  
 DB 16 ALRGVTDFSGFGRADAEVLKRAKMGIGTDEDSITLNLTAASNORQOIAEFTPLFG 75  
 QY 62 DLVNDKMSSELTGFEKELIVALKMPSRLYDAVELKAKLGAGTDEKYLEIIASRTPEEL 121  
 DB 76 DLVNDKMSSELTGFEKELIVALKMPSRLYDAVELKAKLGAGTDEKYLEIIASRTPEEL 135  
 QY 122 RAIKQAYEEYGSNLEDVVDGTSGYQRMVLVLLQANRPPDAIDAQVELDAQLFQA 181  
 DB 136 RAIKQAYEEYGSNLEDVVDGTSGYQRMVLVLLQANRPPDAIDAQVELDAQLFQA 195  
 QY 182 ELKMGIDEEKFTITLIGRSVSHLRVFDKMTISGQIETIDRETSGLNELLAAVVK 241  
 DB 196 ELKMGIDEEKFTITLIGRSVSHLRVFDKMTISGQIETIDRETSGLNELLAAVVK 255



QY 1 MALRGVTDPGSGPGRADAEVLRKAMKGLGTDSDSIINLTARSNARQCIAEFFKTLFG 60  
 Db 1 MALRGVTDPGSGPGRADAEVLRKAMKGLGTDSDSIINLTARSNARQCIAEFFKTLFG 60  
 QY 61 RDVNDMKSSELTGFEKLIYALMKPSRLYDAVELKAKLGAGTDEKVLTEIIASRTPEEL 120  
 Db 61 RDVNDMKSSELTGFEKLIYALMKPSRLYDAVELKAKLGAGTDEKVLTEIIASRTPEEL 120  
 QY 121 RAIKQAYEEYGSNLEDDVYGTSGYQRMVLVLLQANRDPDAIDDAQVELDAQALFOA 180  
 Db 121 RAIKQAYEEYGSNLEDDVYGTSGYQRMVLVLLQANRDPDAIDDAQVELDAQALFOA 180  
 QY 181 GELKMGTDDEKFTITLGTSSVSHLRVFDKMTISGFQIEETIDRETSGNLEILLAVVK 240  
 Db 181 GELKMGTDDEKFTITLGTSSVSHLRVFDKMTISGFQIEETIDRETSGNLEILLAVVK 240  
 QY 241 SIRSIPIAYLAETLYYAMKAGTDDHTLIRIVSRSEIDLFNIRKEFRKNFATSLYSMTKG 300  
 Db 241 SIRSIPIAYLAETLYYAMKAGTDDHTLIRIVSRSEIDLFNIRKEFRKNFATSLYSMTKG 300  
 QY 301 DTSGDYKKAALLLCGGEDD 319  
 Db 301 DTSGDYKKAALLLCGGEDD 319

RESULT 5  
 AAY13924  
 ID AAY13924 standard; protein, 319 AA.

XX AC AAY13924;  
 DT 13-JUN-1999 (first entry)  
 DE S65T GFP variant/hannexin V protein.  
 XX KW GFP; green fluorescent protein; annexin; fusion protein; apoptosis;  
 KW fluorescent intensity; anionic phospholipid binding affinity;  
 KW asymmetric distribution; plasma membrane phospholipid;  
 KW apoptotic cell detection.  
 XX OS Aequorea victoria.  
 OS Homo sapiens.  
 XX OS Synthetic.  
 XX PN WO919470-A2.  
 XX PD 22-APR-1999.  
 XX PF 09-OCT-1998; 98WO-US21444.  
 XX PR 09-OCT-1997; 97US-0948276.  
 XX PA (REGC ) UNIV CALIFORNIA.  
 XX PI Ernst JD;  
 XX DR WPI: 1999-277634/23.  
 XX PT Bifunctional fusion protein useful for the detection of apoptotic  
 PT cells  
 PS Claim 2; Page 15-17; 23pp; English.  
 CC This sequence represents an example of a protein of the invention.  
 CC The proteins are bifunctional Aequorea victoria green fluorescent protein  
 CC (GFP)-annexin fusion proteins, where the GFP and annexin moieties provide  
 CC greater or equal fluorescent intensity and anionic phospholipid binding  
 CC affinity, respectively, than do the corresponding unfused GFP and annexin  
 CC proteins. An early manifestation of apoptosis is the loss of the  
 CC asymmetric distribution of plasma membrane phospholipids, which results  
 CC in exposure of anionic phospholipids on the extracellular leaflet of the  
 CC plasma membrane. The GFP-annexin V fusion proteins are used for the  
 CC detection of apoptotic cells by flow cytometry or fluorescent microscopy.

CC The fusion proteins provide for homogeneously labelled annexin, with  
 CC fluorescence properties that do not change upon binding membrane  
 CC phospholipids, unlike prior art FITC-labelled annexins, where quenching  
 CC of FITC-annexin V fluorescence by 40-50% occurs upon binding phospholipid  
 CC membranes.  
 XX  
 SQ Sequence 319 AA;

Query Match 96.1%; Score 1535; DB 20; Length 319;  
 Best Local Similarity 95.3%; Pred. No. 7,le-129;  
 Matches 304; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 MALRGVTDPGSGPGRADAEVLRKAMKGLGTDSDSIINLTARSNARQCIAEFFKTLFG 60  
 Db 1 MALRGVTDPGSGPGRADAEVLRKAMKGLGTDSDSIINLTARSNARQCIAEFFKTLFG 60  
 QY 61 RDVNDMKSSELTGFEKLIYALMKPSRLYDAVELKAKLGAGTDEKVLTEIIASRTPEEL 120  
 Db 61 RDVNDMKSSELTGFEKLIYALMKPSRLYDAVELKAKLGAGTDEKVLTEIIASRTPEEL 120  
 QY 121 RAIKQAYEEYGSNLEDDVYGTSGYQRMVLVLLQANRDPDAIDDAQVELDAQALFOA 180  
 Db 121 RAIKQAYEEYGSNLEDDVYGTSGYQRMVLVLLQANRDPDAIDDAQVELDAQALFOA 180  
 QY 181 GELKMGTDDEKFTITLGTSSVSHLRVFDKMTISGFQIEETIDRETSGNLEILLAVVK 240  
 Db 181 GELKMGTDDEKFTITLGTSSVSHLRVFDKMTISGFQIEETIDRETSGNLEILLAVVK 240  
 QY 241 SIRSIPIAYLAETLYYAMKAGTDDHTLIRIVSRSEIDLFNIRKEFRKNFATSLYSMTKG 300  
 Db 241 SIRSIPIAYLAETLYYAMKAGTDDHTLIRIVSRSEIDLFNIRKEFRKNFATSLYSMTKG 300  
 QY 301 DTSGDYKKAALLLCGGEDD 319  
 Db 301 DTSGDYKKAALLLCGGEDD 319

## RESULT 6

ABB57067  
 ID ABB57067 standard; protein, 319 AA.

XX AC ABB57067;  
 DT 07-MAR-2002 (first entry)  
 DE Mouse ischaemic condition related protein sequence SEQ ID NO:136.  
 XX KW Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;  
 KW vasospastic ischaemia; ischaemic condition; ischaemic disease.  
 XX OS Mus musculus.  
 XX PN WO200189188-A2.  
 XX PD 22-NOV-2001.  
 XX PF 18-MAY-2001; 2001WO-JP04192.  
 XX PR 18-MAY-2000; 2000JP-0145977.  
 XX PA (UNIV-) UNIV NITHON SCHOOL JURIDICAL PERSON.  
 XX PI Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;  
 XX DR N-PSDB; AB199289.  
 XX PT Examining the ischemic condition (e.g. occlusive ischemia) by measuring  
 PT expression levels of particular genes defined in the specification or  
 PT by determining the expression profile of a gene group comprising these  
 PT genes -  
 XX  
 PS Claim 2; Page 419-421; 2690pp; English.

XX The present invention describes a method for examining ischaemic  
 CC conditions, comprising measuring the expression levels of particular  
 CC genes (I) in a test sample or determining the expression profile of a  
 CC gene group in the sample comprising genes selected from (I). The method  
 CC is useful for examining the ischaemic condition (e.g. compressive  
 CC ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring  
 CC expression levels of particular genes (AB199202 to AB199912, encoding  
 CC the protein sequences in AB197020 to AB197374) or by determining the  
 CC expression profile of a gene group comprising these genes. The  
 CC expression levels or expression profiles produced by these genes are  
 CC used as an indicator when screening for ischaemic condition-improving  
 CC drugs or therapeutics for ischaemic diseases. AB199913 and AB199914  
 CC represent PCR primers for a mouse ischaemic condition related sequence,  
 CC which are used in the exemplification of the present invention.

XX Sequence 319 AA;

Query Match 96.1%; Score 1535; DB 23; Length 319;  
 Best Local Similarity 95.3%; Pred. No. 7, 1e-129;  
 Matches 304; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 MALRGVTDFSGFGDADAEVLRKAMKGLGTDEDSILNLLTARSNAQSQIAEFKTLFG 60  
 Db 1 MATRGVTDFPGFDRADAEVLRKAMKGLGTDEDSILNLLTARSNAQSQIAEFKTLFG 60  
 QY 61 RDLVNDKSELTKGFEKLIVALMKPSRLYDAYELKHAKLGAGTDEKVLTEIIASRTPBEL 120  
 Db 61 RDLVNDKSELTKGFEKLIVALMKPSRLYDAYELKHAKLGAGTDEKVLTEIIASRTPBEL 120  
 QY 121 RAIKQAYEEYSGNLEDDVVGDTSGYQGMVLVLLQANRPDPDAIDQAVEIDQALFOAG 180  
 Db 121 SAIKQAYEEYSGNLEDDVVGDTSGYQGMVLVLLQANRPDPDAIDQAVEIDQALFOAG 180  
 QY 181 GEIKMGDEKFTTIGTSVSHLRVPDKYWTISGFQIEETIDETSQNLLENLLAVYK 240  
 Db 181 GEIKMGDEKFTTIGTSVSHLRVPDKYWTISGFQIEETIDETSQNLLENLLAVYK 240  
 QY 241 SIRSIPAYLAETLYYAMKAGTDHDLIRVIVSRSEIDLFNIRKEFRKNFATSLYSMTKG 300  
 Db 241 SIRSIPAYLAETLYYAMKAGTDHDLIRVIVSRSEIDLFNIRKEFRKNFATSLYSMTKG 300  
 QY 301 DTSGDYKALLLLCGGEDD 319  
 Db 301 DTSGDYKALLLLCGGEDD 319

RESULT 7

AA426276 standard; protein; 319 AA.

XX AAR26276;  
 AC AAR26276;  
 XX 10-MAR-2003 (updated)  
 DT 04-FEB-1993 (first entry)  
 XX CPB-I.  
 DE CPB-I.  
 XX CPB-I; stabilisation; frozen; molten; processed; activity.  
 KM Homo sapiens.  
 OS Homo sapiens.  
 XX JP04198195-A.  
 PN 17-JUL-1992.  
 XX 28-NOV-1990; 90JP-0328286.  
 PF 28-NOV-1990; 90JP-0328286.  
 XX 28-NOV-1990; 90JP-0328286.  
 PR (KAGA ) KAGAKU OYOBI KESSEI RYOH.  
 PA (KOMA ) KOMA CO LTD.  
 XX (KOMA ) KOMA CO LTD.  
 PA (KOMA ) KOMA CO LTD.  
 XX (KOMA ) KOMA CO LTD.

DR WPI; 1992-288937/35.  
 XX Stabilisation of CPB-I for drug compsn. - by adding basic  
 PT aminoacid selected from lysine, arginine and/or ornithine  
 XX  
 XX Disclosure: Page 2; 4pp; Japanese.

XX The sequence given is the amino acid sequence of CPB-I. CPB-I was  
 CC used within a method which involved adding basic amino acids to it  
 CC which resulted in its stabilisation. This lead to the production of  
 CC CPB-I which keeps its activity when it is frozen, molten or has been  
 CC processed by several procedures.  
 CC (updated on 10-MAR-2003 to add missing OS field.)

XX Sequence 319 AA;

Query Match 90.8%; Score 1451.5; DB 13; Length 319;  
 Best Local Similarity 91.5%; Pred. No. 2, 1e-121;  
 Matches 290; Conservative 12; Mismatches 14; Indels 1; Gaps 1;

QY 3 LRGTVDPSGFGDADAEVLRKAMKGLGTDEDSILNLLTARSNAQSQIAEFKTLFGND 62  
 Db 4 LRGTVDPSGFGDADAEVLRKAMKGLGTDEDSILNLLTARSNAQSQIAEFKTLFGND 63  
 QY 63 LVNDKSELTKGFEKLIVALMKPSRLYDAYELKHAKLGAGTDEKVLTEIIASRTPBELRA 122  
 Db 64 LVNDKSELTKGFEKLIVALMKPSRLYDAYELKHAKLGAGTDEKVLTEIIASRTPBELRA 123  
 QY 123 IKQAYEEYSGNLEDDVVGDTSGYQGMVLVLLQANRPDPDAIDQAVEIDQALFOAGE 182  
 Db 124 IKQAYEEYSGNLEDDVVGDTSGYQGMVLVLLQANRPDPDAIDQAVEIDQALFOAGE 183  
 QY 183 LKMGDEKFTTIGTSVSHLRVPDKYWTISGFQIEETIDETSQNLLENLLAVYKSI 242  
 Db 184 LKMGDEKFTTIGTSVSHLRVPDKYWTISGFQIEETIDETSQNLLENLLAVYKSI 243  
 QY 243 RSIPAYLAETLYYAMKAGTDHDLIRVIVSRSEIDLFNIRKEFRKNFATSLYSMTKGD 302  
 Db 244 RSIPAYLAETLYYAMKAGTDHDLIRVIVSRSEIDLFNIRKEFRKNFATSLYSMTKGD 303  
 QY 303 SGGDYKALLLLCGGEDD 319  
 Db 304 SGGDYKALLLLC-GEED 319

RESULT 8

AA41021 standard; protein; 319 AA.

XX AAR41021;  
 AC AAR41021;  
 XX 29-MAR-1994 (first entry)  
 DT 29-MAR-1994 (first entry)  
 XX Calphobindin I (CPB-I).  
 DE Calphobindin I (CPB-I).  
 XX Calphobindin I; CPB-I; Protein kinase C; PKC; inhibition; tumour.  
 KM Homo sapiens.  
 OS Homo sapiens.  
 XX JP05213769-A.  
 PN 24-AUG-1993.  
 XX 04-FEB-1992; 92JP-0019032.  
 PF 04-FEB-1992; 92JP-0019032.  
 XX 04-FEB-1992; 92JP-0019032.  
 PR (KOMA ) KOMA CO LTD.  
 PA (KAGA-) ZH KAGAKU OYOBI KESSEN RYOH KENKUTUSHO.  
 XX WPI; 1993-299558/38.  
 DR Protein kinase C inhibitor effective against malignant tumours -  
 XX

PT contg. (opt. recombinant) calphobindin I  
 XX  
 PS Claim 1; Page 2-3; 6pp; Japanese.  
 XX  
 CC Calphobindin I (CPB-I) or recombinant calphobindin I (r-CPB-I)  
 CC inhibits protein kinase C (PKC) and is useful in the treatment of  
 CC malignant tumours caused by abnormal activation of PKC. CPB-I is  
 CC extracted from human or animal organs and may be applied  
 CC intravenously, orally, intramuscularly, percutaneously or rectally.  
 XX  
 SQ Sequence 319 AA;  
 Query Match 90.8%; Score 1451.5; DB 14; Length 319;  
 Best Local Similarity 91.5%; Pred. No. 2.1e-121;  
 Matches 290; Conservative 12; Mismatches 14; Indels 1; Gaps 1;  
 QY 3 LRGTVDTSFGPDADAEVLKRAMKGLGTDEDSILNLTARSNAQROQIAEFKTLFGD 62  
 DB 4 LRGTVDTSFGPDADAEVLKRAMKGLGTDEDSILNLTARSNAQROQIAEFKTLFGD 63  
 QY 63 LVNDKSELTKGFEKLIYALMKPSRLYDAYELKXAKLQAGTDEKLTETIISRTPEERA 122  
 DB 64 LDDDKSELTKGFEKLIYALMKPSRLYDAYELKXAKLQAGTDEKLTETIISRTPEERA 123  
 QY 123 IKQAYEEYGSNLEDDVVDGTSGYQRMVLVLLQANRPPDAIDDAQVELDAQALFOAGE 182  
 DB 124 IKQAYEEYGSNLEDDVVDGTSGYQRMVLVLLQANRPPDAIDDAQVELDAQALFOAGE 183  
 QY 183 LKMGTEDEKFTITLGRSVSHLRVPDKYMTISGFIETIDRETSGLNLELLAVVSI 242  
 DB 184 LKMGTEDEKFTITLGRSVSHLRVPDKYMTISGFIETIDRETSGLNLELLAVVSI 243  
 QY 243 RSIPAYIAETLYYAMKAGTDHTLIRIVSRSEIDLFNIRKEFRKPAFSLYSMTIKGDT 302  
 DB 244 RSIPAYIAETLYYAMKAGTDHTLIRIVSRSEIDLFNIRKEFRKPAFSLYSMTIKGDT 303  
 QY 303 SGDYKXALLLCCGEDD 319  
 DB 304 SGDYKXALLLCCGEDD 319  
 RESULT 9  
 ABG32550  
 ID ABG32550 standard; protein; 319 AA.  
 AC ABG32550;  
 XX  
 DT 29-NOV-2002 (first entry)  
 XX  
 DE Human CPB-1 protein.  
 XX  
 KW Human; CPB-I; eye drop; ophthalmological; anexin V; corneal disease;  
 KW calcium/phospholipid binding protein; polyhydric alcohol.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200267977-A1.  
 XX  
 PD 06-SEP-2002.  
 XX  
 PF 21-FEB-2002; 2002WO-JP01563.  
 XX  
 PR 26-FEB-2001; 2001JP-0050297.  
 XX  
 PA (KOWA ) KOWA CO LTD.  
 PA (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.  
 PI Naruse H, Sano M, Shinoda Y, Inagi T;  
 XX  
 DR WPI; 2002-674988/72.  
 XX  
 PT Eye drops for treating e.g. corneal diseases, contain CPB-I and  
 PT polyhydric alcohol with specific carbonyl value, without unpleasant

PT irritation upon dropping but with satisfactory long-term storability  
 XX  
 PS Disclosure; Page 13-14; 16pp; Japanese.  
 XX  
 CC The invention relates to eye drops contain CPB-I (anexin V) and a  
 CC polyhydric alcohol having a carbonyl value of not more than  
 CC 5mlcr0 Mol/5. The eye drops are for treating e.g. corneal diseases.  
 CC Such eye drops are without unpleasant irritation upon dropping but with  
 CC satisfactory long-term storage stability. The present sequence is  
 CC the human CPB-I (calcium/phospholipid binding) protein.  
 XX  
 SQ Sequence 319 AA;  
 Query Match 90.8%; Score 1451.5; DB 23; Length 319;  
 Best Local Similarity 91.5%; Pred. No. 2.1e-121;  
 Matches 290; Conservative 12; Mismatches 14; Indels 1; Gaps 1;  
 QY 3 LRGTVDTSFGPDADAEVLKRAMKGLGTDEDSILNLTARSNAQROQIAEFKTLFGD 62  
 DB 4 LRGTVDTSFGPDADAEVLKRAMKGLGTDEDSILNLTARSNAQROQIAEFKTLFGD 63  
 QY 63 LVNDKSELTKGFEKLIYALMKPSRLYDAYELKXAKLQAGTDEKLTETIISRTPEERA 122  
 DB 64 LDDDKSELTKGFEKLIYALMKPSRLYDAYELKXAKLQAGTDEKLTETIISRTPEERA 123  
 QY 123 IKQAYEEYGSNLEDDVVDGTSGYQRMVLVLLQANRPPDAIDDAQVELDAQALFOAGE 182  
 DB 124 IKQAYEEYGSNLEDDVVDGTSGYQRMVLVLLQANRPPDAIDDAQVELDAQALFOAGE 183  
 QY 183 LKMGTEDEKFTITLGRSVSHLRVPDKYMTISGFIETIDRETSGLNLELLAVVSI 242  
 DB 184 LKMGTEDEKFTITLGRSVSHLRVPDKYMTISGFIETIDRETSGLNLELLAVVSI 243  
 QY 243 RSIPAYIAETLYYAMKAGTDHTLIRIVSRSEIDLFNIRKEFRKPAFSLYSMTIKGDT 302  
 DB 244 RSIPAYIAETLYYAMKAGTDHTLIRIVSRSEIDLFNIRKEFRKPAFSLYSMTIKGDT 303  
 QY 303 SGDYKXALLLCCGEDD 319  
 DB 304 SGDYKXALLLCCGEDD 319  
 RESULT 10  
 AAP80511  
 ID AAP80511 standard; protein; 320 AA.  
 AC AAP80511;  
 XX  
 DT 25-MAR-2003 (updated)  
 DT 10-MAR-2003 (updated)  
 DT 12-NOV-1990 (first entry)  
 XX  
 DE Placental coagulation inhibitor.  
 XX  
 KW Placental coagulation inhibitor; disseminated vascular coagulation;  
 KW thrombosis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP279459-A.  
 PN JP03219875-A.  
 XX  
 PD 24-AUG-1988.  
 XX  
 PF 19-FEB-1988; 88EP-0102468.  
 XX  
 PR 20-FEB-1987; 87JP-0037227.  
 PR 23-JUL-1987; 87JP-0184428.  
 XX  
 PA (KOWA ) KOWA CO LTD.  
 PI Sano Y, Iwasaki A, Suda M;  
 XX

DR WPI, 1988-236733/34.  
 DR WPI, 1991-329110/45.  
 DR N-PSDB; AAN81113.  
 XX Recombinant placental coagulation inhibitor - useful for the prevention  
 PT and treatment of thromboses or disseminated intra-vascular coagulation.  
 XX  
 PS Disclosure; Page 7; ?pp; English.  
 XX  
 CC This polypeptide exhibits strong anticoagulant activities and is useful  
 CC for the treatment and prevention of e.g. thrombosis or disseminated  
 CC intravascular coagulation in the brain, heart and peripheral blood  
 CC vessels, such as cerebral and myocardial infarction. It has no  
 CC antigenicity against man and can be produced in large amounts using  
 CC recombinant methods.  
 CC (Updated on 10-MAR-2003 to add missing OS field.)  
 CC (Updated on 25-MAR-2003 to correct PF field.)  
 CC (Updated on 25-MAR-2003 to correct PR field.)  
 CC (Updated on 25-MAR-2003 to correct PA field.)  
 XX  
 SQ Sequence 320 AA;  
 Query Match 90.8%; Score 1451.5; DB 9; Length 320;  
 Best Local Similarity 91.5%; Pred. No. 2.1e-121;  
 Matches 290; Conservative 12; Mismatches 14; Indels 1; Gaps 1;  
 QY 3 LRGTVTDFSGFGRADAETLRKAMKGLGTDDESIINLTARSNAQROQIAEEFTLFGRD 62  
 Db 5 LRGTVTDFSGFGRADAETLRKAMKGLGTDDESIINLTARSNAQROQIAEEFTLFGRD 64  
 QY 63 LVNDKSELTGKFEKLIYALMKPSRLYDAYELKAKLGAQDEKVTETIIASRTPEELRA 122  
 Db 65 LDDDLKSELTGKFEKLIYALMKPSRLYDAYELKAKLGAQDEKVTETIIASRTPEELRA 124  
 QY 123 IKQAYEEYSGNLEDDVGDTSQYQRMVLVLLQANRDPDTAIDDAQVELDAQALFQAGE 182  
 Db 125 IKQAYEEYSGNLEDDVGDTSQYQRMVLVLLQANRDPDTAIDDAQVELDAQALFQAGE 184  
 QY 183 LKMGTDDEKFTITLGRSVSHLRVDFKXMTISGFOIEETIDRETSGNLEMLLAAYKSI 242  
 Db 185 LKMGTDDEKFTITLGRSVSHLRVDFKXMTISGFOIEETIDRETSGNLEMLLAAYKSI 244  
 QY 243 RSIPIAYLAETLYYAMKAGTDHTLIRVYSRSEIDLFNIRKEPRKXFASTLYSMIKGDT 302  
 Db 245 RSIPIAYLAETLYYAMKAGTDHTLIRVYSRSEIDLFNIRKEPRKXFASTLYSMIKGDT 304  
 QY 303 SGDYKKALLLCCGEDD 319  
 Db 305 SGDYKKALLLCCGEDD 320  
 RESULT 11  
 AAP91953  
 ID AAP91953 standard; protein; 320 AA.  
 XX  
 AC AAP91953;  
 XX  
 DT 25-MAR-2003 (updated)  
 DT 10-MAR-2003 (updated)  
 DT 30-JUL-1989 (first entry)  
 XX  
 DS Vascular anti-coagulating protein-alpha.  
 XX  
 KM Vascular anti-coagulating proteins; hybridomas; B-cells; myelomas.  
 XX  
 OS Chimeric - Homo sapiens.  
 OS Chimeric - Mus musculus.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..320  
 XX /product=VAC-alpha protein  
 PN DE3810331-A.

XX  
 PD 05-OCT-1989.  
 XX  
 PF 26-MAR-1988; 88DE-3810331.  
 XX  
 PR 26-MAR-1988; 88DE-3810331.  
 XX  
 XX (BOEH) BOEHRINGER INGELHEIM.  
 PA  
 XX  
 PI Gunther A;  
 XX  
 DR WPI, 1989-293724/41.  
 DR N-PSDB; AAN91353.  
 XX  
 PT Monoclonal antibodies to vascular anti-coagulating proteins - and  
 PT hybridomas producing such antibodies.  
 XX  
 PS Disclosure; fig 1; 11pp; German.  
 XX  
 CC This vascular anti-coagulating protein (VAC)-alpha is used in the  
 CC preparation of monoclonal antibodies (Vabs). The VAC-alpha is injected  
 CC into a host animal, in conjugation with eg keyhole limpet haemocyanin,  
 CC and the B-cells from immunised hosts are then fused with myeloma cells.  
 CC The resultant hybridomas (VAA-8 and VAA-9) produce Abs specific to VAC-  
 CC alpha. Abs can be used as immunoassay reagents to detect VAC proteins,  
 CC as affinity ligands for protein purification, and as medicaments for binding  
 CC and/or neutralising VAC proteins in vivo. See also AAN91354 and  
 CC EP-181465.  
 CC (Updated on 10-MAR-2003 to add missing OS field.)  
 CC (Updated on 25-MAR-2003 to correct PA field.)  
 XX  
 SQ Sequence 320 AA;  
 Query Match 90.8%; Score 1451.5; DB 10; Length 320;  
 Best Local Similarity 91.5%; Pred. No. 2.1e-121;  
 Matches 290; Conservative 12; Mismatches 14; Indels 1; Gaps 1;  
 QY 3 LRGTVTDFSGFGRADAETLRKAMKGLGTDDESIINLTARSNAQROQIAEEFTLFGRD 62  
 Db 5 LRGTVTDFSGFGRADAETLRKAMKGLGTDDESIINLTARSNAQROQIAEEFTLFGRD 64  
 QY 63 LVNDKSELTGKFEKLIYALMKPSRLYDAYELKAKLGAQDEKVTETIIASRTPEELRA 122  
 Db 65 LDDDLKSELTGKFEKLIYALMKPSRLYDAYELKAKLGAQDEKVTETIIASRTPEELRA 124  
 QY 123 IKQAYEEYSGNLEDDVGDTSQYQRMVLVLLQANRDPDTAIDDAQVELDAQALFQAGE 182  
 Db 125 IKQAYEEYSGNLEDDVGDTSQYQRMVLVLLQANRDPDTAIDDAQVELDAQALFQAGE 184  
 QY 183 LKMGTDDEKFTITLGRSVSHLRVDFKXMTISGFOIEETIDRETSGNLEMLLAAYKSI 242  
 Db 185 LKMGTDDEKFTITLGRSVSHLRVDFKXMTISGFOIEETIDRETSGNLEMLLAAYKSI 244  
 QY 243 RSIPIAYLAETLYYAMKAGTDHTLIRVYSRSEIDLFNIRKEPRKXFASTLYSMIKGDT 302  
 Db 245 RSIPIAYLAETLYYAMKAGTDHTLIRVYSRSEIDLFNIRKEPRKXFASTLYSMIKGDT 304  
 QY 303 SGDYKKALLLCCGEDD 319  
 Db 305 SGDYKKALLLCCGEDD 320  
 RESULT 12  
 AAR13082  
 ID AAR13082 standard; Protein; 320 AA.  
 XX  
 AC AAR13082;  
 XX  
 DT 25-MAR-2003 (updated)  
 DT 30-SEP-1991 (first entry)  
 XX  
 DE PAP-I.



KW Phospholipid; binding protein; lipocortin; domain; vitamin K; PBP;  
 KW gla-domain; VKDP.  
 XX Homo sapiens.  
 OS WO9109953-A.  
 PN 11-JUL-1991.  
 XX  
 XX PD 13-DEC-1990; 90WO-US07335.  
 XX PR 29-DEC-1989; 89US-0459082.  
 XX PA (ZYMO ) ZYMOGENETICS INC.  
 XX PI Foster DC;  
 XX DR WPI; 1991-222905/30.  
 DR N-PSDB; AAQ12679.  
 XX  
 XX PT Recombinant prodn. of hybrid phospholipid-binding proteins -  
 PT comprising lipocortin phospholipid-binding domain and  
 PT vitamin K-dependent protein  
 XX  
 XX PS Disclosure; Fig 7; 57pp; English.  
 CC This sequence, or a fragment of it, is used in the construction of  
 CC hybrid phospholipid-binding proteins (PBP) comprising at least one  
 CC lipocortin phospholipid binding domain (PBD), e.g. of PBP-1, joined  
 CC to a gla-domainless vitamin K-dependent protein, e.g. protein C or  
 CC activated protein C. See AAQ12679-81 for such examples.  
 CC (Updated on 25-MAR-2003 to correct PA field.)  
 CC  
 CC SQ Sequence 320 AA;  
 Query Match 90.8%; Score 1451.5; DB 12; Length 320;  
 Best Local Similarity 91.5%; Pred. No. 2.1e-121;  
 Matches 290; Conservative 12; Mismatches 14; Indels 1; Gaps 1;  
 QY 3 LRGIYDFSGFDGRADAEVLKRAKAGLGTDEDSILNLTARSNAORQOIAEEFKTLFGRD 62  
 DB 5 LRGIYDFSGFDGRADAEVLKRAKAGLGTDEDSILNLTARSNAORQOIAEEFKTLFGRD 64  
 QY 63 LVNDKSELTKGFEKLIYALMKPSRLYDAYELKAKAGLGTDEKVTETIISRPEELRA 122  
 DB 65 LDDDKSELTKGFEKLIYALMKPSRLYDAYELKAKAGLGTDEKVTETIISRPEELRA 124  
 QY 123 IKQAYEEYGSNLEDDVVGDTSGYYQRMVLVLLQANRPDPTAIDDAQVELDAQALFQAGE 182  
 DB 125 IKQAYEEYGSNLEDDVVGDTSGYYQRMVLVLLQANRPDPTAIDDAQVELDAQALFQAGE 184  
 QY 163 LKMGTDDEKFTITLIGTRSVSHLRKVPDKMTISGFOIEETIDRETSGNLENLLAVVXSI 242  
 DB 165 LKMGTDDEKFTITLIGTRSVSHLRKVPDKMTISGFOIEETIDRETSGNLENLLAVVXSI 244  
 QY 243 RSIPAYLAETLYYAMKAGAGTDHTLIRIVSRSEIDLFNIRKFRKNFATSLYSWIKGDT 302  
 DB 245 RSIPAYLAETLYYAMKAGAGTDHTLIRIVSRSEIDLFNIRKFRKNFATSLYSWIKGDT 304  
 QY 303 SGDIYKALLLLCGGDD 319  
 DB 305 SGDIYKALLLLCGGDD 320  
 RESULT 13  
 AA13923  
 ID AA13923 standard; protein, 320 AA.  
 XX  
 XX AC AA13923;  
 XX  
 XX DT 13-JUL-1999 (first entry)  
 XX

DE S65T GFP variant/annexin V protein.  
 KW GFP; green fluorescent protein; annexin; fusion protein; apoptosis;  
 KW fluorescent intensity; anionic phospholipid binding affinity;  
 KW asymmetric distribution; plasma membrane phospholipid;  
 KW apoptotic cell detection.  
 XX  
 XX OS Aegeorea victoria.  
 OS Homo sapiens.  
 OS Synthetic.  
 XX WO9119470-A2.  
 XX PD 22-APR-1999.  
 XX PR 09-OCT-1998; 98WO-US21444.  
 XX PA (REGC ) UNIV CALIFORNIA.  
 XX PI Ernst JD;  
 XX DR WPI; 1999-277634/23.  
 XX  
 XX PT Bifunctional fusion protein useful for the detection of apoptotic  
 PT cells  
 XX  
 XX PS Claim 2; Page 14-15; 23pp; English.  
 CC This sequence represents an example of a protein of the invention.  
 CC The proteins are bifunctional Aegeorea victoria green fluorescent protein  
 CC (GFP)-annexin fusion proteins, where the GFP and annexin moieties provide  
 CC greater or equal fluorescent intensity and anionic phospholipid binding  
 CC affinity, respectively, than do the corresponding unfused GFP and annexin  
 CC proteins. An early manifestation of apoptosis is the loss of the  
 CC asymmetric distribution of plasma membrane phospholipids, which results  
 CC in exposure of anionic phospholipids on the extracellular leaflet of the  
 CC plasma membrane. The GFP-annexin V fusion proteins are used for the  
 CC detection of apoptotic cells by flow cytometry or fluorescent microscopy.  
 CC The fusion proteins provide for homogeneously labelled annexin, with  
 CC fluorescence properties that do not change upon binding membrane  
 CC phospholipids, unlike prior art FITC-labelled annexins, where quenching  
 CC of FITC-annexin V fluorescence by 40-50% occurs upon binding phospholipid  
 CC membranes.  
 CC  
 CC SQ Sequence 320 AA;  
 Query Match 90.8%; Score 1451.5; DB 20; Length 320;  
 Best Local Similarity 91.5%; Pred. No. 2.1e-121;  
 Matches 290; Conservative 12; Mismatches 14; Indels 1; Gaps 1;  
 QY 3 LRGIYDFSGFDGRADAEVLKRAKAGLGTDEDSILNLTARSNAORQOIAEEFKTLFGRD 62  
 DB 5 LRGIYDFSGFDGRADAEVLKRAKAGLGTDEDSILNLTARSNAORQOIAEEFKTLFGRD 64  
 QY 63 LVNDKSELTKGFEKLIYALMKPSRLYDAYELKAKAGLGTDEKVTETIISRPEELRA 122  
 DB 65 LDDDKSELTKGFEKLIYALMKPSRLYDAYELKAKAGLGTDEKVTETIISRPEELRA 124  
 QY 123 IKQAYEEYGSNLEDDVVGDTSGYYQRMVLVLLQANRPDPTAIDDAQVELDAQALFQAGE 182  
 DB 125 IKQAYEEYGSNLEDDVVGDTSGYYQRMVLVLLQANRPDPTAIDDAQVELDAQALFQAGE 184  
 QY 163 LKMGTDDEKFTITLIGTRSVSHLRKVPDKMTISGFOIEETIDRETSGNLENLLAVVXSI 242  
 DB 165 LKMGTDDEKFTITLIGTRSVSHLRKVPDKMTISGFOIEETIDRETSGNLENLLAVVXSI 244  
 QY 243 RSIPAYLAETLYYAMKAGAGTDHTLIRIVSRSEIDLFNIRKFRKNFATSLYSWIKGDT 302  
 DB 245 RSIPAYLAETLYYAMKAGAGTDHTLIRIVSRSEIDLFNIRKFRKNFATSLYSWIKGDT 304  
 QY 303 SGDIYKALLLLCGGDD 319

Db 305 SGDYKALLLLC-GEED 320

RESULT 14  
ID AAY84788 standard; peptide; 320 AA.  
XX AAY84788;  
XX  
XX  
XX 08-AUG-2000 (first entry)  
XX  
XX Amino acid sequence of annexin V.  
XX  
XX Annexin; phospholipid; antithrombotic; antitumor; antiinflammatory;  
XX coating; thrombogenic biomaterial; labelling compound; negative charge.  
XX  
XX Unidentified.  
XX  
XX Key Location/Qualifiers  
XX Domain 16..31  
XX /note= "domain 1"  
XX  
XX FR2784106-A1.  
XX  
XX 07-APR-2000.  
XX  
XX 02-OCT-1998; 98FR-0012366.  
XX  
XX 02-OCT-1998; 98FR-0012366.  
XX  
XX (COMS ) COMMISSARIAT ENERGIE ATOMIQUE.  
XX (UYPA-) UNIV CURIE PARIS VI P & M.  
XX  
XX Sanson A, Rosso MF, Neumann JM, Cordier OF, Guerois R;  
XX  
XX WPI; 2000-320664/28.  
XX  
XX  
XX Chemical structure having affinity for phospholipid comprises chemical  
XX platform comprising six residues supporting set of chemical functions  
XX that are capable of binding to phospholipid  
XX  
XX  
XX Claim 13; Fig 6b; 63pp; French.  
XX  
XX The present sequence represents an annexin polypeptide. The domain of  
XX annexin, which may be modified, is used to construct the chemical  
XX compounds of the invention. The specification describes chemical  
XX compounds which have an affinity for a phospholipid. The chemical  
XX compounds comprise at least one chemical platform comprising six  
XX residues supporting a set of chemical functions that are capable of  
XX binding to the phospholipid and at least partly define the affinity  
XX of the structure for the phospholipid. The compounds act as  
XX phospholipid sequestrers. The compounds are useful for preparing  
XX antithrombotic, antitumor and antiinflammatory medicaments, for  
XX making coatings for thrombogenic biomaterials, and for preparing  
XX labelling compounds useful for analysing and detecting negative  
XX charges on cell surfaces and microvesicles in blood.  
XX  
XX  
XX Sequence 320 AA;  
XX  
XX  
XX Query March 90.8%; Score 1451.5; DB 21; Length 320;  
XX Best Local Similarity 91.5%; Match No. 2.1e-121;  
XX Matches 290; Conservative 12; Mismatches 14; Indels 1; Gaps 1;  
XX  
XX  
XX 3 LRGVTDPSGFDGRADAEVLRKAMKGLGTDEDSIINLTLPASNAQRQIAEEFKTLFGRD 62  
XX 5 LRGVTDPSGFDGRADAEVLRKAMKGLGTDEDSIINLTLPASNAQRQIAEEFKTLFGRD 64  
XX  
XX 63 LINDMKSELTKGEKKIVALKMPSRLVDAYELKHAELGSGTEKVLTEIISRPEEIRA 122  
XX 65 LINDMKSELTKGEKKIVALKMPSRLVDAYELKHAELGSGTEKVLTEIISRPEEIRA 124  
XX  
XX 123 IKAAYEEYGSNLEDDVVGDTSGYORMLVLLQANRPDPAIDDAOVELDPAQALFOAGE 182

Db 305 SGDYKALLLLC-GEED 320

RESULT 15  
ID ABG31220 standard; Protein; 320 AA.  
XX ABG31220;  
XX  
XX 05-NOV-2002 (first entry)  
XX  
XX Human annexin V, containing a delta RACK binding site.  
XX  
XX Human; annexin V; delta RACK; delta protein kinase C; deltaPKC;  
XX VI domain; vasotrophic; cerebroprotective; delatavi-1; delatavi-2; RACK;  
XX pseudo-delta RACK; pseudo-delta receptor for activated C-kinase;  
XX delatavi-5; PKC; protein kinase C; signal transduction; cell growth;  
XX gene expression; ion channel activity; translocation; hypoxia; stroke;  
XX ischaemic damage; creatine kinase.  
XX  
XX  
XX Homo sapiens.  
XX  
XX WO200257413-A2.  
XX  
XX 25-JUL-2002.  
XX  
XX 09-NOV-2001; 2001WO-US47556.  
XX  
XX 18-JUN-2001; 2001US-262060P.  
XX  
XX (STRD ) UNIV LELAND STANFORD JUNIOR.  
XX  
XX Mochly-Rosen D;  
XX  
XX WPI; 2002-559715/64.  
XX  
XX  
XX New delta protein kinase C peptide for reducing or enhancing damage to  
XX cells or tissues exposed to ischemic or hypoxic event caused by stroke,  
XX or for protecting tissue from damage due to ischemia  
XX  
XX  
XX Claim 45; Page 64-65; 65pp; English.  
XX  
XX The invention discloses peptides comprising delatavi-1, delatavi-2,  
XX pseudo-delta receptors for activated C-kinase (RACK), delatavi-5 or their  
XX derivatives or fragments. Protein kinase C (PKC) is a key enzyme in  
XX signal transduction involved in a variety of cellular functions including  
XX cell growth, regulation of gene expression and ion channel activity. The  
XX localisation of different PKC isozymes to different areas of the cell in  
XX turn appears due to binding of the activated isozymes to the specific  
XX anchoring molecules (RACKs). Peptides that mimic either the PKC-binding  
XX site on RACKs or the RACK-binding site on PKC are isozyme specific  
XX translocation inhibitors of PKC. The disclosed peptides are useful in  
XX activating or inhibiting translocation or function of deltaPKC. The  
XX deltaPKC agonists or antagonists are useful in reducing, enhancing or  
XX protecting against damage to cells or tissues due to ischemic or hypoxic  
XX event caused by stroke. Acute administration of the peptides, conjugated  
XX to a carrier peptide or a Tat-derived peptide, protected hearts against  
XX ischemic damage as shown by decreased release of creatine kinase. The  
XX data indicate that in an intact heart, inhibition of deltaPKC conferred  
XX greater than 50% protection against ischaemic damage. The sequence

CC presented is human annexin V, which contains a delta RACK binding site.

XX Sequence 320 AA;

Query Match 90.8%; Score 1451.5; DB 23; Length 320;

Best Local Similarity 91.5%; Pred. No. 2.1e-121;

Matches 290; Conservative 12; Mismatches 14; Indels 1; Gaps 1;

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QY 3 LRGTVDSSGPDGRADAVLRKAKKGLTDEDSIANLLTARSNAQRQQAIEFKTLFGRD 62
   |||||
DB 5 LRGTVDPPGFDERADAEFLRKAKKGLTDEESITLTLTSRNAQRQQAIEFKTLFGRD 64
   |||||
QY 63 LVNDKSELTKGFEKLIYALMKPSRLYDAVELKAKLAGTDEKVLTEIIASRTPELRA 122
   |||||
DB 65 LLDLKSSELTKGFEKLIYALMKPSRLYDAVELKAKLAGTNEKVLTEIIASRTPELRA 124
   |||||
QY 123 IKQAYEEBYGSLNEDVVGDTSGYQRMVYLQANRDPDTAIDDAQVELDAQALFOAGE 182
   |||||
DB 125 IKQAYEEBYGSLNEDVVGDTSGYQRMVYLQANRDPDAGIDEAQVEBODACALFOAGE 184
   |||||
QY 183 LKMGIDEKFFITLIGTRSVSHLRVFDKMTISGFOIETITIDETSQNLLENLLAVVXSI 242
   |||||
DB 185 LKMGIDEKFFITIGTRSVSHLRVFDKMTISGFOIETITIDETSQNLLENLLAVVXSI 244
   |||||
QY 243 RSIPAYLAETLYYANKAGTDDATLIRIVRSSEIDLFNIRKEFRKPFATSLYSMTKSDT 302
   |||||
DB 245 RSIPAYLAETLYYANKAGTDDATLIRIVRSSEIDLFNIRKEFRKPFATSLYSMTKSDT 304
   |||||
QY 303 SGDYKKAALLLCGGEDD 319
   |||||
DB 305 SGDYKKAALLLC-GEDD 320
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Search completed: December 12, 2003, 14:50:02  
Job time : 26.8613 secs



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; Patent No. 5849600
; GENERAL INFORMATION:
; APPLICANT: Nixon, Ralph
; TITLE OF INVENTION: DIAGNOSTIC ASSAYS FOR ALZHEIMER'S
; TITLE OF INVENTION: DISEASE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/149,975A
; FILING DATE: 11-NOV-1993
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 04843/016001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 319 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-149-975A-2

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Query Match          98.6%; Score 1575; DB 2; Length 319;
Best Local Similarity 98.7%; Pred. No. 8.5e-149;
Matches 315; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MALRGVTDPGSGFDGRADAEVLKRAMKGLGTDEDSILNLTARSNARQQAEEFTLFG 60
DB 1 MALRGVTDPGSGFDGRADAEVLKRAMKGLGTDEDSILNLTARSNARQQAEEFTLFG 60
QY 61 RDLVNDKSELTKGFEKLIYALMKPSRLYDAYELKHALKGAGTDEKVTLEIIASRTPEEL 120
DB 61 RDLVNDKSELTKGFEKLIYALMKPSRLYDAYELKHALKGAGTDEKVTLEIIASRTPEEL 120
QY 121 RAIKQAYEEYGSNLIEDVVDGTSYQRMVLVLQANRDPPTAIDDAQVELDAQALFQA 180
DB 121 RAIKQAYEEYGSNLIEDVVDGTSYQRMVLVLQANRDPPTAIDDAQVELDAQALFQA 180
QY 181 GELKMGTDSEKFTITIGTSVSHLRVFDKMTISGFISETIDRETSNLEMLLAVVK 240
DB 181 GELKMGTDSEKFTITIGTSVSHLRVFDKMTISGFISETIDRETSNLEMLLAVVK 240
QY 241 SIRSIPAYLAETLYYAMKAGTDDHTLIRVVSSEIDLFINRKEFRKPFATSLYSMTKG 300
DB 241 SIRSIPAYLAETLYYAMKAGTDDHTLIRVVSSEIDLFINRKEFRKPFATSLYSMTKG 300
QY 301 DTSGDYKKALLLLCGGEDD 319
DB 301 DTSGDYKKALLLLCGGEDD 319

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```

RESULT 3
US-08-948-276-2
; Sequence 2, Application US/08948276
; Patent No. 6511829

```

```

; GENERAL INFORMATION:
; APPLICANT: Ernst, Joel D.
; TITLE OF INVENTION: GFP-Annexin Fusion Proteins
; FILE REFERENCE: USF97-113
; CURRENT APPLICATION NUMBER: US/08/948,276
; CURRENT FILING DATE: 1997-10-09
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 319
; TYPE: PRT
; ORGANISM: mouse
; US-08-948-276-2

Query Match          96.1%; Score 1535; DB 4; Length 319;
Best Local Similarity 95.3%; Pred. No. 8.2e-145;
Matches 304; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 MALRGVTDPGSGFDGRADAEVLKRAMKGLGTDEDSILNLTARSNARQQAEEFTLFG 60
DB 1 MALRGVTDPGSGFDGRADAEVLKRAMKGLGTDEDSILNLTARSNARQQAEEFTLFG 60
QY 61 RDLVNDKSELTKGFEKLIYALMKPSRLYDAYELKHALKGAGTDEKVTLEIIASRTPEEL 120
DB 61 RDLVNDKSELTKGFEKLIYALMKPSRLYDAYELKHALKGAGTDEKVTLEIIASRTPEEL 120
QY 121 RAIKQAYEEYGSNLIEDVVDGTSYQRMVLVLQANRDPPTAIDDAQVELDAQALFQA 180
DB 121 SAIKQAYEEYGSNLIEDVVDGTSYQRMVLVLQANRDPPTAIDDAQVELDAQALFQA 180
QY 181 GELKMGTDSEKFTITIGTSVSHLRVFDKMTISGFISETIDRETSNLEMLLAVVK 240
DB 181 GELKMGTDSEKFTITIGTSVSHLRVFDKMTISGFISETIDRETSNLEMLLAVVK 240
QY 241 SIRSIPAYLAETLYYAMKAGTDDHTLIRVVSSEIDLFINRKEFRKPFATSLYSMTKG 300
DB 241 SIRSIPAYLAETLYYAMKAGTDDHTLIRVVSSEIDLFINRKEFRKPFATSLYSMTKG 300
QY 301 DTSGDYKKALLLLCGGEDD 319
DB 301 DTSGDYKKALLLLCGGEDD 319

RESULT 4
US-08-125-746-1
; Sequence 1, Application US/08125746
; Patent No. 5531633
; GENERAL INFORMATION:
; APPLICANT: SAINO, YUSHI
; APPLICANT: IMASAKI, AKIO
; APPLICANT: SUDA, MAKOTO
; TITLE OF INVENTION: ANTICOAGULANT POLYPEPTIDE
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/125,746
; FILING DATE: 24-SEP-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/807,623
; FILING DATE: 13-DEC-1991

```

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 037227/1987  
FILING DATE: 20-FEB-1987  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 184428/1987  
FILING DATE: 23-JUL-1987  
ATTORNEY/AGENT INFORMATION:  
NAME: O'Brien, No. 559163man F.  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 80-074-0 DIV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 413-3000  
TELEFAX: (703) 413-2220  
TELEX: 248855 OPAT UR  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 319 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
US-08-125-746-1

Query Match 90.8%; Score 1451.5; DB 1; Length 319;  
Best Local Similarity 91.5%; Pred. No. 1.7e-136;  
Matches 290; Conservative 12; Mismatches 14; Indels 1; Gaps 1;

QY 3 LRGTYDPSGFDGRDAEVLRRKMKGLGTDSDSILNLTARNAQROQIAEPPKTLFGRD 62  
DB 4 LRGTYDPSGFDGRDAEVLRRKMKGLGTDSDSILNLTARNAQROQIAEPPKTLFGRD 63  
QY 63 LVNDKMSSELTKGFEKILVALMKPSRLYDAVELKAKLGAAGDEVLLEIIASRPEELRA 122  
DB 64 LVNDKMSSELTKGFEKILVALMKPSRLYDAVELKAKLGAAGDEVLLEIIASRPEELRA 123  
QY 123 IKQAYEEYGSNLEDDVVGDTSGYQRMVLLQANRDPDAIDDAQVELDAQALFQAGE 182  
DB 124 IKQAYEEYGSNLEDDVVGDTSGYQRMVLLQANRDPDAIDDAQVELDAQALFQAGE 183  
QY 183 LKMGDDEKFTITLGRSVSHLRKVFQDKYMTISGFQIEETIDRETSGNLEIIASRPEELRA 242  
DB 184 LKMGDDEKFTITLGRSVSHLRKVFQDKYMTISGFQIEETIDRETSGNLEIIASRPEELRA 243  
QY 243 RSIPIVLAETLYYAKKAGTDDHTLIRVYRSSEIDLFINRKEFRKNFATSLYSMIKGD 302  
DB 244 RSIPIVLAETLYYAKKAGTDDHTLIRVYRSSEIDLFINRKEFRKNFATSLYSMIKGD 303  
QY 303 SGDYKXALLLCGGEDD 319  
DB 304 SGDYKXALLLC-GEED 319

RESULT 5  
US-08-125-746-3  
Sequence 3, Application US/08125746  
Patent No. 5591633  
GENERAL INFORMATION:  
APPLICANT: SAINO, YUSHI  
APPLICANT: IMASAKI, AKIO  
APPLICANT: SUDA, MAKOTO  
TITLE OF INVENTION: ANTICOAGULANT POLYPEPTIDE  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: OBION, SPIVAK, MCLELLAND, MAIER & NEUSTADT,  
ADDRESSEE: P.C.  
STREET: 1755 S. Jefferson Davis Highway, Suite 400  
CITY: Arlington  
STATE: Virginia  
COUNTRY: U.S.A.  
ZIP: 22202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/125,746  
FILING DATE: 24-SEP-1993  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/807,623  
FILING DATE: 13-DEC-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 037227/1987  
FILING DATE: 20-FEB-1987  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 184428/1987  
FILING DATE: 23-JUL-1987  
ATTORNEY/AGENT INFORMATION:  
NAME: O'Brien, No. 559163man F.  
REGISTRATION NUMBER: 24,618  
REFERENCE/DOCKET NUMBER: 80-074-0 DIV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 413-3000  
TELEFAX: (703) 413-2220  
TELEX: 248855 OPAT UR  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 320 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-125-746-3

Query Match 90.8%; Score 1451.5; DB 1; Length 320;  
Best Local Similarity 91.5%; Pred. No. 1.7e-136;  
Matches 290; Conservative 12; Mismatches 14; Indels 1; Gaps 1;

QY 3 LRGTYDPSGFDGRDAEVLRRKMKGLGTDSDSILNLTARNAQROQIAEPPKTLFGRD 62  
DB 5 LRGTYDPSGFDGRDAEVLRRKMKGLGTDSDSILNLTARNAQROQIAEPPKTLFGRD 64  
QY 63 LVNDKMSSELTKGFEKILVALMKPSRLYDAVELKAKLGAAGDEVLLEIIASRPEELRA 122  
DB 65 LVNDKMSSELTKGFEKILVALMKPSRLYDAVELKAKLGAAGDEVLLEIIASRPEELRA 124  
QY 123 IKQAYEEYGSNLEDDVVGDTSGYQRMVLLQANRDPDAIDDAQVELDAQALFQAGE 182  
DB 125 IKQAYEEYGSNLEDDVVGDTSGYQRMVLLQANRDPDAIDDAQVELDAQALFQAGE 184  
QY 183 LKMGDDEKFTITLGRSVSHLRKVFQDKYMTISGFQIEETIDRETSGNLEIIASRPEELRA 242  
DB 185 LKMGDDEKFTITLGRSVSHLRKVFQDKYMTISGFQIEETIDRETSGNLEIIASRPEELRA 244  
QY 243 RSIPIVLAETLYYAKKAGTDDHTLIRVYRSSEIDLFINRKEFRKNFATSLYSMIKGD 302  
DB 245 RSIPIVLAETLYYAKKAGTDDHTLIRVYRSSEIDLFINRKEFRKNFATSLYSMIKGD 304  
QY 303 SGDYKXALLLCGGEDD 319  
DB 305 SGDYKXALLLC-GEED 320

RESULT 6  
US-08-948-276-1  
Sequence 1, Application US/08948276  
Patent No. 6511829  
GENERAL INFORMATION:  
APPLICANT: Ernst, Joel D.  
TITLE OF INVENTION: GFP-AnneXin Fusion Proteins  
FILE REFERENCE: US97-113  
CURRENT APPLICATION NUMBER: US/08/948,276  
CURRENT FILING DATE: 1997-10-09  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 1  
LENGTH: 320

TYPE: PRT  
ORGANISM: human  
US-08-948-276-1

Query Match 90.8%; Score 1451.5; DB 4; Length 320;  
Best Local Similarity 91.5%; Pred. No. 1.7e-136;  
Matches 290; Conservative 12; Mismatches 14; Indels 1; Gaps 1;

QY 3 LRGTVDPSGFDGADAEVLRKMKKGLTDEDSILNLTARSNAQOQIAEFKTLFGD 62  
DB 5 LRGTVDPSGFDGADAEVLRKMKKGLTDEDSILNLTARSNAQOQIAEFKTLFGD 64  
QY 63 LVNDKSELTKGFEKLIYALMKPSRLYDAYELKAKLGAAGTDEKVLTEIIASRTPPELRA 122  
DB 65 LDDDKSELTKGFEKLIYALMKPSRLYDAYELKAKLGAAGTDEKVLTEIIASRTPPELRA 124  
QY 123 IKQAYEEYSGNLEDDVVDGTSYQRMVLVLLQANRDPDAIDDAQVELDAQALFOAGE 182  
DB 125 IKQAYEEYSGNLEDDVVDGTSYQRMVLVLLQANRDPDAIDDAQVELDAQALFOAGE 184  
QY 183 LKMGDEEKFITITGTRSVSHLRVPDKYMTISGFOIETIDRETSGNLENLLAVKSI 242  
DB 185 LKMGDEEKFITITGTRSVSHLRVPDKYMTISGFOIETIDRETSGNLENLLAVKSI 244  
QY 243 RSIPIAYLAETLYYAMKAGTDDHTLIRVIVSRSEIDLFNIRKEFRNPAFSLYSMIKQDT 302  
DB 245 RSIPIAYLAETLYYAMKAGTDDHTLIRVIVSRSEIDLFNIRKEFRNPAFSLYSMIKQDT 304  
QY 303 SCDYKKAALLLGCGEDD 319  
DB 305 SCDYKKAALLLGCGEDD 320

RESULT 7  
522537-4  
Patent No. 522537  
APPLICANT: FOSTER, DONALD  
TITLE OF INVENTION: METHODS FOR PRODUCING HYBRID  
PHOSPHOLIPID-BINDING PROTEINS  
NUMBER OF SEQUENCES: 14  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/459, 082  
FILING DATE: 29-DEC-1989  
SEQ ID NO: 4  
LENGTH: 320  
522537-4

Query Match 90.8%; Score 1451.5; DB 6; Length 320;  
Best Local Similarity 91.5%; Pred. No. 1.7e-136;  
Matches 290; Conservative 12; Mismatches 14; Indels 1; Gaps 1;

QY 3 LRGTVDPSGFDGADAEVLRKMKKGLTDEDSILNLTARSNAQOQIAEFKTLFGD 62  
DB 5 LRGTVDPSGFDGADAEVLRKMKKGLTDEDSILNLTARSNAQOQIAEFKTLFGD 64  
QY 63 LVNDKSELTKGFEKLIYALMKPSRLYDAYELKAKLGAAGTDEKVLTEIIASRTPPELRA 122  
DB 65 LDDDKSELTKGFEKLIYALMKPSRLYDAYELKAKLGAAGTDEKVLTEIIASRTPPELRA 124  
QY 123 IKQAYEEYSGNLEDDVVDGTSYQRMVLVLLQANRDPDAIDDAQVELDAQALFOAGE 182  
DB 125 IKQAYEEYSGNLEDDVVDGTSYQRMVLVLLQANRDPDAIDDAQVELDAQALFOAGE 184  
QY 183 LKMGDEEKFITITGTRSVSHLRVPDKYMTISGFOIETIDRETSGNLENLLAVKSI 242  
DB 185 LKMGDEEKFITITGTRSVSHLRVPDKYMTISGFOIETIDRETSGNLENLLAVKSI 244  
QY 243 RSIPIAYLAETLYYAMKAGTDDHTLIRVIVSRSEIDLFNIRKEFRNPAFSLYSMIKQDT 302  
DB 245 RSIPIAYLAETLYYAMKAGTDDHTLIRVIVSRSEIDLFNIRKEFRNPAFSLYSMIKQDT 304  
QY 303 SCDYKKAALLLGCGEDD 319  
DB 305 SCDYKKAALLLGCGEDD 320

DB 305 SCDYKKAALLLGCGEDD 320

RESULT 8  
US-09-324-096A-2  
Sequence 2, Application US/09324096A  
Patent No. 632313  
GENERAL INFORMATION:  
APPLICANT: Tait, Jonathan  
TITLE OF INVENTION: ANNEXIN DERIVATIVE WITH ENDOGENOUS CHELATION SITES  
FILE REFERENCE: US/09-324, 096A  
CURRENT APPLICATION NUMBER: US/09/324, 096A  
CURRENT FILING DATE: 1999-06-01  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 2  
LENGTH: 327  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-324-096A-2

Query Match 90.3%; Score 1442.5; DB 4; Length 327;  
Best Local Similarity 91.2%; Pred. No. 1.4e-135;  
Matches 289; Conservative 12; Mismatches 15; Indels 1; Gaps 1;

QY 3 LRGTVDPSGFDGADAEVLRKMKKGLTDEDSILNLTARSNAQOQIAEFKTLFGD 62  
DB 12 LRGTVDPSGFDGADAEVLRKMKKGLTDEDSILNLTARSNAQOQIAEFKTLFGD 71  
QY 63 LVNDKSELTKGFEKLIYALMKPSRLYDAYELKAKLGAAGTDEKVLTEIIASRTPPELRA 122  
DB 72 LDDDKSELTKGFEKLIYALMKPSRLYDAYELKAKLGAAGTDEKVLTEIIASRTPPELRA 131  
QY 123 IKQAYEEYSGNLEDDVVDGTSYQRMVLVLLQANRDPDAIDDAQVELDAQALFOAGE 182  
DB 132 IKQAYEEYSGNLEDDVVDGTSYQRMVLVLLQANRDPDAIDDAQVELDAQALFOAGE 191  
QY 183 LKMGDEEKFITITGTRSVSHLRVPDKYMTISGFOIETIDRETSGNLENLLAVKSI 242  
DB 192 LKMGDEEKFITITGTRSVSHLRVPDKYMTISGFOIETIDRETSGNLENLLAVKSI 251  
QY 243 RSIPIAYLAETLYYAMKAGTDDHTLIRVIVSRSEIDLFNIRKEFRNPAFSLYSMIKQDT 302  
DB 252 RSIPIAYLAETLYYAMKAGTDDHTLIRVIVSRSEIDLFNIRKEFRNPAFSLYSMIKQDT 311  
QY 303 SCDYKKAALLLGCGEDD 319  
DB 312 SCDYKKAALLLGCGEDD 327

RESULT 9  
US-09-324-096A-4  
Sequence 4, Application US/09324096A  
Patent No. 632313  
GENERAL INFORMATION:  
APPLICANT: Tait, Jonathan  
TITLE OF INVENTION: ANNEXIN DERIVATIVE WITH ENDOGENOUS CHELATION SITES  
FILE REFERENCE: US/09-324, 096A  
CURRENT APPLICATION NUMBER: US/09/324, 096A  
CURRENT FILING DATE: 1999-06-01  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 4  
LENGTH: 327  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-324-096A-4

Query Match 90.3%; Score 1442.5; DB 4; Length 327;  
Best Local Similarity 91.2%; Pred. No. 1.4e-135;  
Matches 289; Conservative 12; Mismatches 15; Indels 1; Gaps 1;





APPLICATION NUMBER: US/08/214,036  
 FILING DATE: 07/837,775  
 APPLICATION NUMBER: 07/837,775  
 FILING DATE: February 13, 1992  
 APPLICATION NUMBER: 07/764,465  
 FILING DATE: September 23, 1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Clark, Paul T.  
 REGISTRATION NUMBER: 30,162  
 REFERENCE/DOCKET NUMBER: 00786/099001  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 542-5070  
 TELEFAX: (617) 542-8906  
 TELEX: 200154  
 INFORMATION FOR SEQ ID NO: 14:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 319  
 TYPE: amino acid  
 STRANDEDNESS: N/A  
 TOPOLOGY: N/A  
 US-08-526-136-14

Query Match 57.3%; Score 916; DB 3; Length 319;  
 Best Local Similarity 57.3%; Pred. No. 4e-83;  
 Matches 180; Conservative 54; Mismatches 80; Indels 0; Gaps 0;

5 GTVDFSGFGADAEVLRKAMKGGTDEDSILNLTARSNAQOQIAEFTLFGDLY 64  
 6 GTVKAASGFNAEDQTLRKAMKGGTDEDAIIVLAVRSRQOELRTAYKTTIGRDL 65  
 65 NDKSELTGKFKELIVALKMPSRLYDAVELKAKLGAGTDEKVTETIASRTPEELRAI 124  
 66 DDKSELGSGNFQVILGNTPTVLDVQELRKAMKGGTDEGCIEIETIASRTPEELRAI 125  
 125 QAYEEYGSNLEDDVVGDTSGYQSMVYLLQANRDPDTAIDAQVELDQALFOAGELK 184  
 126 QYVQOQYGSLEDDVRSPTSEMFQRYVLSLSAGRDSNVIDDLAKQDQDYKAGEKK 185  
 185 WGTDEKFTTLIGTRSVSHLRVPDKYVTISGFOIETITRETSNLENLLAVKXIRS 244  
 186 WGTDEVKFTLVCSNRRHLJHFEDEYRIQAKXIEQISKETSSEDALLAIVKCMEN 245  
 245 IYAVLAETLYYAMKAGDHDITLRVYSRSEIDLFNIRKFRKNFATSLYSMTKGDTS 304  
 246 KSAVFAERLYYKMKGLGTDITLIRVWVSRAIDMLDIRANFKLYGKSLYSPIKGDTS 305  
 305 DYKALLLLCGGED 318  
 306 DYRKVLLILCGGD 319

RESULT 13  
 US-08-526-136-2  
 Sequence 2, Application US/08526136  
 Patent No. 6107089  
 GENERAL INFORMATION:  
 APPLICANT: Towle, Christine A. et al.  
 TITLE OF INVENTION: ANNEXIN XI  
 NUMBER OF SEQUENCES: 36  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Fish & Richardson  
 STREET: 225 Franklin Street  
 CITY: Boston  
 STATE: Massachusetts  
 COUNTRY: U.S.A.  
 ZIP: 02110-2804  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
 COMPUTER: IBM PS/2 Model 502 or 55SX  
 OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)  
 SOFTWARE: WordPerfect (Version 5.0)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/526,136

FILING DATE: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/214,036  
 FILING DATE:  
 APPLICATION NUMBER: 07/837,775  
 FILING DATE: February 13, 1992  
 APPLICATION NUMBER: 07/764,465  
 FILING DATE: September 23, 1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Clark, Paul T.  
 REGISTRATION NUMBER: 30,162  
 REFERENCE/DOCKET NUMBER: 00786/099001  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617) 542-5070  
 TELEFAX: (617) 542-8906  
 TELEX: 200154  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 503  
 TYPE: amino acid  
 TOPOLOGY: N/A  
 US-08-526-136-2

Query Match 54.4%; Score 870; DB 3; Length 503;  
 Best Local Similarity 55.6%; Pred. No. 3.1e-78;  
 Matches 175; Conservative 54; Mismatches 86; Indels 0; Gaps 0;

4 RGTDFSGFGADAEVLRKAMKGGTDEDSILNLTARSNAQOQIAEFTLFGDLY 63  
 189 RGTIDASGFPDPRDLEVLKAMKGGTDEQAIIDLSGRSKQOQLSTFKIVGDL 248  
 64 VNDKSELTKFKELIVALKMPSRLYDAVELKAKLGAGTDEKVTETIASRTPEELRAI 123  
 249 IKDKSELGSGNFQVILGNTPTVLDVQELRKAMKGGTDEGCIEIETIASRTPEELRAI 125  
 124 QAYEEYGSNLEDDVVGDTSGYQSMVYLLQANRDPDTAIDAQVELDQALFOAGEL 184  
 309 NRYVKTFTKLEEARSDTSGHFORLLISLQGRDSTNVDMLVQDVELYAAEN 368  
 184 KWTDEKFTTLIGTRSVSHLRVPDKYVTISGFOIETITRETSNLENLLAVKXIRS 243  
 369 RLGDESKFTALICSNRHLLVAVFNEYQRMGRDIKSIKEMSGDLEQGLAVKCLX 428  
 244 SIPVLAETLYYAMKAGDHDITLRVYSRSEIDLFNIRKFRKNFATSLYSMTKGDTS 303  
 429 NTPAFFAERLYYKMKGLGTDITLIRVWVSRAIDMLDIRANFKLYGKSLYHDTGDS 488  
 304 GDYKALLLLCGGED 318  
 489 GDYRKILLIKCGGD 503

RESULT 14  
 US-08-526-136-4  
 Sequence 4, Application US/08526136  
 Patent No. 6107089  
 GENERAL INFORMATION:  
 APPLICANT: Towle, Christine A. et al.  
 TITLE OF INVENTION: ANNEXIN XI  
 NUMBER OF SEQUENCES: 36  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Fish & Richardson  
 STREET: 225 Franklin Street  
 CITY: Boston  
 STATE: Massachusetts  
 COUNTRY: U.S.A.  
 ZIP: 02110-2804  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
 COMPUTER: IBM PS/2 Model 502 or 55SX  
 OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)  
 SOFTWARE: WordPerfect (Version 5.0)

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/526,136
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/214,036
FILING DATE:
APPLICATION NUMBER: 07/837,775
FILING DATE: February 13, 1992
APPLICATION NUMBER: 07/764,465
FILING DATE: September 23, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/099001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 505
TYPE: amino acid
TOPOLOGY: N/A
US-08-526-136-4

Query Match      54.4%; Score 870; DB 3; Length 505;
Best Local Similarity 55.6%; Pred. No. 3.1e-78;
Matches 175; Conservative 54; Mismatches 86; Indels 0; Gaps 0;

QY 4 RGVITDFSGFDGRADAEVLARKAMKGLGTDSDIINLLTARSNAQRQIAEEFKTLFGDRL 63
Db 191 RGVITDASGFDPLRADAVLARKAMKGFDTGQALIDCLGSRSMKQROQILLSFKTAYGKDL 250

QY 64 VNMKSELTGKFEKLIYALMKPSRLYDAVELKAKLAGTDEKVLTEIIASRTPEELRAI 123
Db 251 IKDKSELSGNFEKTLIYALMKPSRLYDAVELKAKLAGTDEKVLTEIIASRTPEELRAI 310

QY 124 KQAYEEVGSNLEDVVDVDTSGYQRMVLVLQANRPDPTAIDDAQVELDAQALFOAGEL 183
Db 311 NRVYKTFEKKTLLEAHSIDTSNGHFORLLISLQGNRDESTNVDMIVQSDVQELYAAGEN 370

QY 184 KMGDEKEFTIIGTSVSHLRVFDKXMTISGFOIEETIDRETSNLENLLAVYSIR 243
Db 371 RLGTDESKFNALICSRRAHLVAVFNEYQPMGTGRDIEKSIQEMSGDLEQGMILAVKCLX 430

QY 244 SIPAYLAETLYYAMKAGTDHTLIRIVYSSEIDLFRIRKPKRNKFNATSLYSMTKSDTS 303
Db 431 NTPAFPAERLAKMKGAGTQDRTILIRIMVSRSEIDLDIRAEYKLYGKSLYHDITGDS 490

QY 304 GDYKALLLLCGGED 318
Db 491 GDYKILLIKICGGND 505

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RESULT 15
US-08-948-276-5
; Sequence 5, Application US/08948276
; Patent No. 6511829
; GENERAL INFORMATION:
; APPLICANT: Ernst, Joel D.
; TITLE OF INVENTION: GFP-AnneXin Fusion Proteins
; FILE REFERENCE: US97-113
; CURRENT APPLICATION NUMBER: US/08/948,276
; CURRENT FILING DATE: 1997-10-09
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 323
; TYPE: PRT
; ORGANISM: human
US-08-948-276-5

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Query Match      49.1%; Score 785; DB 4; Length 323;
Best Local Similarity 48.3%; Pred. No. 4.6e-70;
Matches 152; Conservative 68; Mismatches 95; Indels 0; Gaps 0;

QY 4 RGVITDFSGFDGRADAEVLARKAMKGLGTDSDIINLLTARSNAQRQIAEEFKTLFGDRL 63
Db 9 RGVITDPPFSVDAEAIQKIRIGIDDEKILSILTERSNARQIIVAEYQAAVYKEL 68

QY 64 VNMKSELTGKFEKLIYALMKPSRLYDAVELKAKLAGTDEKVLTEIIASRTPEELRAI 123
Db 69 KDLKGDLSGHEHLMVALVTPPAVFDKQKSKMKGAGTNEALRIELTTRTSRQKDI 128

QY 124 KQAYEEVGSNLEDVVDVDTSGYQRMVLVLQANRPDPTAIDDAQVELDAQALFOAGEL 183
Db 129 SQAYTVYKKSIGDDISSETSGDFKALLTLADGRDSSLKVDEHLAKQDAQILYVAGEN 188

QY 184 KMGDEKEFTIIGTSVSHLRVFDKXMTISGFOIEETIDRETSNLENLLAVYSIR 243
Db 189 RMGTDEKFTTELCLRSFPQKLTDEYRNISQKDIYDSIKGELSGHPEDLILAVNCR 248

QY 244 SIPAYLAETLYYAMKAGTDHTLIRIVYSSEIDLFRIRKPKRNKFNATSLYSMTKSDTS 303
Db 249 NTPAFPAERLAKMKGAGTQDRTILIRIMVSRSEIDLDIRAEYKLYGKSLYHDITGDS 308

QY 304 GDYKALLLLCGGED 318
Db 309 GDYETILLIKICGGD 323

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Search completed: December 12, 2003, 14:53:23  
Job time: 10.6862 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 12, 2003, 14:50:08 ; Search time 17.7581 Seconds  
(without alignments)  
3340.943 Million cell updates/sec

Title: PCT-US03-24332-3

Perfect score: 1598  
Sequence: 1 MALRGVTVDPSGFDGRADAE.....GDTSGDYKALLLCGGED 319

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 694280 seqs, 185983659 residues

Total number of hits satisfying chosen parameters: 694280

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Published Applications\_AA.\*  
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2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
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18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1598	100.0	319	12 US-10-080-370-3	Sequence 3, Appl1
9	1593	99.7	669	12 US-10-080-370-6	Sequence 6, Appl1
3	1451.5	90.8	320	14 US-10-007-761-72	Sequence 72, Appl1
4	1442.5	90.3	327	10 US-09-970-969-2	Sequence 2, Appl1
5	1442.5	90.3	327	10 US-09-970-969-4	Sequence 4, Appl1
6	1442.5	90.3	327	10 US-09-970-969-6	Sequence 6, Appl1
7	921	57.6	321	15 US-10-097-340-10	Sequence 10, Appl1
8	921	57.6	324	9 US-09-925-301-1062	Sequence 1062, Ap
9	886	55.4	208	9 US-09-925-302-731	Sequence 731, Ap
10	822.5	51.5	327	12 US-10-216-031B-18	Sequence 18, Appl
11	787	49.2	324	12 US-10-316-253-262	Sequence 262, Appl
12	787	49.1	323	15 US-10-205-823-24	Sequence 34, Appl
13	760	47.6	485	10 US-09-925-300-1664	Sequence 1664, Ap
14	695.5	43.5	339	10 US-09-974-298-91	Sequence 91, Appl
15	695.5	43.5	339	15 US-10-097-340-6	Sequence 6, Appl1

16	695.5	43.5	339	15 US-10-097-340-8	Sequence 8, Appl1
17	678	42.4	327	9 US-09-764-853-615	Sequence 615, App
18	675	42.2	332	11 US-09-764-881-110	Sequence 110, App
19	647.5	40.5	319	15 US-10-304-287-2	Sequence 2, Appl1
20	622	36.9	373	9 US-09-925-301-868	Sequence 868, App
21	618	36.7	346	10 US-09-919-172-39	Sequence 39, Appl
22	618	36.7	346	10 US-09-974-298-93	Sequence 93, Appl
23	615	36.5	346	12 US-10-316-253-300	Sequence 300, App
24	381.5	23.9	289	9 US-09-925-301-897	Sequence 897, App
25	376.5	23.6	316	15 US-10-219-220-260	Sequence 260, App
26	374.5	23.4	316	15 US-10-219-220-62	Sequence 62, Appl
27	315	19.7	158	9 US-09-925-297-479	Sequence 479, App
28	237.5	14.9	239	15 US-10-219-220-65	Sequence 65, Appl
29	223.5	14.0	319	12 US-10-259-165-56	Sequence 56, Appl
30	223.5	14.0	319	12 US-10-259-165-402	Sequence 402, App
31	221	13.8	184	15 US-10-219-220-66	Sequence 66, Appl
32	218	13.6	336	12 US-10-259-165-290	Sequence 290, App
33	139	8.7	82	9 US-09-925-301-1467	Sequence 1467, Ap
34	132	7.6	46	12 US-10-029-386-30160	Sequence 30160, A
35	114	7.1	111	15 US-10-219-220-63	Sequence 63, Appl
36	111.5	7.0	1051	10 US-09-911-888-13	Sequence 14, Appl
37	109	6.8	591	9 US-09-815-242-5837	Sequence 5837, A
38	109	6.8	701	9 US-09-815-242-13002	Sequence 13002, A
39	105	6.6	73	15 US-10-219-220-64	Sequence 64, Appl
40	105	6.6	365	11 US-09-809-391-696	Sequence 696, App
41	105	6.6	365	12 US-09-882-171-696	Sequence 696, App
42	103.5	6.5	662	11 US-09-951-051A-141	Sequence 141, App
43	99	6.2	617	9 US-09-815-242-13228	Sequence 13228, A
44	98.5	6.2	483	12 US-10-316-253-8	Sequence 8, Appl1
45	98	6.1	315	9 US-09-925-301-1053	Sequence 1053, Ap

## ALIGNMENTS

RESULT 1  
US-10-080-370-3  
; Sequence 3, Application US/10080370  
; Publication No. US20030166532A1  
; GENERAL INFORMATION:  
; APPLICANT: Allison, Anthony  
; TITLE OF INVENTION: Modified Annexin Proteins and Methods for Preventing Thrombosis  
; FILE REFERENCE: SURR.90  
; CURRENT APPLICATION NUMBER: US/10/080.370  
; PRIOR FILING DATE: 2002-02-21  
; PRIOR APPLICATION NUMBER: 60/270,402  
; PRIOR FILING DATE: 2001-02-21  
; PRIOR APPLICATION NUMBER: 60/332,582  
; PRIOR FILING DATE: 2001-11-21  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 319  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-080-370-3

Query Match 100.0%; Score 1598; DB 12; Length 319;  
Best Local Similarity 100.0%; Pred. No. 3, 4e-142;  
Matches 319; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
DB 121 RAIKAYEEFGNSLDEDDVVDITGTYQRMVLVLLQNNRDPDPAIDDAQVELDAQALFOA 180  
121 RAIKAYEEFGNSLDEDDVVDITGTYQRMVLVLLQNNRDPDPAIDDAQVELDAQALFOA 180

QY 181 GELKMGDEEKFITLLGTRSVSHLRVFDKMTISGFOIETTIDRETSQNLNLLAVYK 240  
DB 181 GELKMGDEEKFITLLGTRSVSHLRVFDKMTISGFOIETTIDRETSQNLNLLAVYK 240  
QY 241 SRSIPAYLAETLYYAMKAGTDHTLIRIVSRSEIDLFNIRKPKNFATSLYSMIKG 300  
DB 241 SRSIPAYLAETLYYAMKAGTDHTLIRIVSRSEIDLFNIRKPKNFATSLYSMIKG 300  
QY 301 DTSGDYKXKALLLCCGSED 319  
DB 301 DTSGDYKXKALLLCCGSED 319

RESULT 2  
US-10-080-370-6  
; Sequence 6, Application US/10080370  
; Publication No. US20030166532A1  
; GENERAL INFORMATION:  
; APPLICANT: Allison, Anthony  
; TITLE OF INVENTION: Modified Annexin Proteins and Methods for Preventing Thrombosis  
; FILE REFERENCE: SURR.90  
; CURRENT APPLICATION NUMBER: US/10/080,370  
; PRIOR FILING DATE: 2002-02-21  
; PRIOR APPLICATION NUMBER: 60/270,402  
; PRIOR FILING DATE: 2001-02-21  
; PRIOR APPLICATION NUMBER: 60/332,582  
; PRIOR FILING DATE: 2001-11-21  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6  
; LENGTH: 669  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; NAME/KEY: misc.feature  
; LOCATION: (15)..(15)  
; OTHER INFORMATION: The 'Xaa' at location 15 stands for Ser.  
; NAME/KEY: misc.feature  
; LOCATION: (334)..(334)  
; OTHER INFORMATION: The 'Xaa' at location 334 stands for Lys, Asn, Arg, Ser, Thr, Ile  
; OTHER INFORMATION: Tyr, Trp, Cys, or Phe.  
; NAME/KEY: misc.feature  
; LOCATION: (351)..(351)  
; OTHER INFORMATION: The 'Xaa' at location 351 stands for Lys, Asn, Arg, Ser, Thr, Ile  
; OTHER INFORMATION: Tyr, Trp, Cys, or Phe.  
; NAME/KEY: misc.feature  
; LOCATION: (45)..(45)  
; OTHER INFORMATION: n = a, c, g, or t  
; NAME/KEY: misc.feature  
; LOCATION: (1000)..(1002)  
; OTHER INFORMATION: n = a, c, g, or t  
; NAME/KEY: misc.feature  
; LOCATION: (1051)..(1053)  
; OTHER INFORMATION: n = a, c, g, or t  
US-10-080-370-6

Query Match 99.7%; Score 1593; DB 12; Length 669;  
Best Local Similarity 100.0%; Freq. No. 3e-141;  
Matches 318; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 ALRGVTDFSGFDGRADAEVLKRMKGLGTDDESIINLTARSNAQROQIAEEFKTLFGF 61  
DB 16 ALRGVTDFSGFDGRADAEVLKRMKGLGTDDESIINLTARSNAQROQIAEEFKTLFGF 75  
QY 62 DIVNDKSELTKFEKFLIYALMKPSRLYDAYELKHAKEAGTDEKVTETIIASRTPEELR 121  
DB 76 DIVNDKSELTKFEKFLIYALMKPSRLYDAYELKHAKEAGTDEKVTETIIASRTPEELR 135  
QY 122 AIKQAYEEYGSNLEDDVVGDTSGYQRMVLVLLQANRPDPTAIDDAQVELDAQALFQAG 181

DB 136 AIKQAYEEYGSNLEDDVVGDTSGYQRMVLVLLQANRPDPTAIDDAQVELDAQALFQAG 195  
QY 182 ELKMGDEEKFITLLGTRSVSHLRVFDKMTISGFOIETTIDRETSQNLNLLAVYK 241  
DB 196 ELKMGDEEKFITLLGTRSVSHLRVFDKMTISGFOIETTIDRETSQNLNLLAVYK 255  
QY 242 IRSIPAYLAETLYYAMKAGTDHTLIRIVSRSEIDLFNIRKPKNFATSLYSMIKG 301  
DB 256 IRSIPAYLAETLYYAMKAGTDHTLIRIVSRSEIDLFNIRKPKNFATSLYSMIKG 315  
QY 302 TSQDYKXKALLLCCGSED 319  
DB 316 TSQDYKXKALLLCCGSED 333

RESULT 3  
US-10-007-761-72  
; Sequence 72, Application US/10007761  
; Publication No. US20020150984A1  
; GENERAL INFORMATION:  
; APPLICANT: Mochly-Rosen, Daria  
; TITLE OF INVENTION: Peptides for Activation and Inhibition  
; FILE REFERENCE: 58600-8208-US00  
; CURRENT APPLICATION NUMBER: US/10/007,761  
; PRIOR FILING DATE: 2001-11-09  
; PRIOR APPLICATION NUMBER: US 60/262,060  
; PRIOR FILING DATE: 2001-01-18  
; NUMBER OF SEQ ID NOS: 72  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 72  
; LENGTH: 320  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-007-761-72

Query Match 90.8%; Score 1451.5; DB 14; Length 320;  
Best Local Similarity 91.5%; Freq. No. 2.1e-126;  
Matches 290; Conservative 12; Mismatches 14; Indels 1; Gaps 1;

QY 3 LRGTVDPFSGFDGRADAEVLKRMKGLGTDDESIINLTARSNAQROQIAEEFKTLFGF 62  
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QY 63 LVNDKSELTKFEKFLIYALMKPSRLYDAYELKHAKEAGTDEKVTETIIASRTPEELR 122  
DB 65 LVNDKSELTKFEKFLIYALMKPSRLYDAYELKHAKEAGTDEKVTETIIASRTPEELR 124  
QY 123 IKQAYEEYGSNLEDDVVGDTSGYQRMVLVLLQANRPDPTAIDDAQVELDAQALFQAG 182  
DB 125 IKQAYEEYGSNLEDDVVGDTSGYQRMVLVLLQANRPDPTAIDDAQVELDAQALFQAG 184  
QY 183 LRKMGDEEKFITLLGTRSVSHLRVFDKMTISGFOIETTIDRETSQNLNLLAVYK 242  
DB 185 LRKMGDEEKFITLLGTRSVSHLRVFDKMTISGFOIETTIDRETSQNLNLLAVYK 244  
QY 243 RSIPAYLAETLYYAMKAGTDHTLIRIVSRSEIDLFNIRKPKNFATSLYSMIKG 302  
DB 245 RSIPAYLAETLYYAMKAGTDHTLIRIVSRSEIDLFNIRKPKNFATSLYSMIKG 304  
QY 303 SGGDYKXKALLLCCGSED 319  
DB 305 SGGDYKXKALLLCCGSED 320

RESULT 4  
US-03-970-969-2  
; Sequence 2, Application US/03970969  
; Patent No. US20020103341A1  
; GENERAL INFORMATION:  
; APPLICANT: Tait, Jonathan F.  
; APPLICANT: Brown, David S.  
; TITLE OF INVENTION: Annexin Derivatives with Endogenous Chelation Sites

FILE REFERENCE: uc0w-1-13841  
 CURRENT APPLICATION NUMBER: US/09/970,969  
 CURRENT FILING DATE: 2001-10-03  
 NUMBER OF SEQ ID NOS: 6  
 SOFTWARE: Patentn Ver. 2.0  
 SEQ ID NO 2  
 LENGTH: 327  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-970-969-2

Query Match 90.3%; Score 1442.5; DB 10; Length 327;  
 Best Local Similarity 91.2%; Pred. No. 1.6e-127;  
 Matches 289; Conservative 12; Mismatches 15; Indels 1; Gaps 1;

QY 3 LRGTVDPSGFDGRADAEVLRKAMKGLGTDEDSILNLTARSNAQROQIAEEFKTLFGSD 62  
 DB 12 LRGTVDPSGFDGRADAEVLRKAMKGLGTDEDSILNLTARSNAQROQISAAFKTLFGSD 71  
 QY 63 LVNDKSELTKGFEKLIYALMKPSRLYDAYELKAKAGAGTDEKVTETIIASRTPPELRA 122  
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 QY 123 IKQAYEEYSGNLEDVVDGTSGYQRMVLLQANRDPDAIDDAQVELDAQALFQAGE 182  
 DB 132 IKQAYEEYSGNLEDVVDGTSGYQRMVLLQANRDPDAIDDAQVELDAQALFQAGE 191  
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 DB 192 LKMGDEBEKFTITLGTSSVSHLRVFDKMTISGFQIETIDRETSNLEMLLAUVKSI 251  
 QY 243 RSIPIAYLAETLYYAMKAGAGTDHDLIRVVSSEIDLFNIRKFRKPFATSLYSMIKSDT 302  
 DB 252 RSIPIAYLAETLYYAMKAGAGTDHDLIRVVSSEIDLFNIRKFRKPFATSLYSMIKSDT 311  
 QY 303 SGDYKXALLLLCGEED 319  
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RESULT 5  
 US-09-970-969-4

Sequence 4, Application US/09970969  
 Patent No. US20020103341A1  
 GENERAL INFORMATION:  
 APPLICANT: Taft, Jonathan F.  
 TITLE OF INVENTION: Annexin Derivatives with Endogenous Chelation Sites  
 FILE REFERENCE: uc0w-1-13841  
 CURRENT APPLICATION NUMBER: US/09/970,969  
 CURRENT FILING DATE: 2001-10-03  
 NUMBER OF SEQ ID NOS: 6  
 SOFTWARE: Patentn Ver. 2.0  
 SEQ ID NO 4  
 LENGTH: 327  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-970-969-4

Query Match 90.3%; Score 1442.5; DB 10; Length 327;  
 Best Local Similarity 91.2%; Pred. No. 1.6e-127;  
 Matches 289; Conservative 12; Mismatches 15; Indels 1; Gaps 1;

QY 3 LRGTVDPSGFDGRADAEVLRKAMKGLGTDEDSILNLTARSNAQROQIAEEFKTLFGSD 62  
 DB 12 LRGTVDPSGFDGRADAEVLRKAMKGLGTDEDSILNLTARSNAQROQISAAFKTLFGSD 71  
 QY 63 LVNDKSELTKGFEKLIYALMKPSRLYDAYELKAKAGAGTDEKVTETIIASRTPPELRA 122  
 DB 72 LLDLKSSELTKGFEKLIYALMKPSRLYDAYELKAKAGAGTDEKVTETIIASRTPPELRA 131  
 QY 123 IKQAYEEYSGNLEDVVDGTSGYQRMVLLQANRDPDAIDDAQVELDAQALFQAGE 182

DB 132 IKQAYEEYSGNLEDVVDGTSGYQRMVLLQANRDPDAIDDAQVELDAQALFQAGE 191  
 QY 183 LKMGDEBEKFTITLGTSSVSHLRVFDKMTISGFQIETIDRETSNLEMLLAUVKSI 242  
 DB 192 LKMGDEBEKFTITLGTSSVSHLRVFDKMTISGFQIETIDRETSNLEMLLAUVKSI 251  
 QY 243 RSIPIAYLAETLYYAMKAGAGTDHDLIRVVSSEIDLFNIRKFRKPFATSLYSMIKSDT 302  
 DB 252 RSIPIAYLAETLYYAMKAGAGTDHDLIRVVSSEIDLFNIRKFRKPFATSLYSMIKSDT 311  
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 DB 312 SGDYKXALLLLCGEED 327

RESULT 6  
 US-09-970-969-6

Sequence 6, Application US/09970969  
 Patent No. US20020103341A1  
 GENERAL INFORMATION:  
 APPLICANT: Taft, Jonathan F.  
 TITLE OF INVENTION: Annexin Derivatives with Endogenous Chelation Sites  
 FILE REFERENCE: uc0w-1-13841  
 CURRENT APPLICATION NUMBER: US/09/970,969  
 CURRENT FILING DATE: 2001-10-03  
 NUMBER OF SEQ ID NOS: 6  
 SOFTWARE: Patentn Ver. 2.0  
 SEQ ID NO 6  
 LENGTH: 327  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-09-970-969-6

Query Match 90.3%; Score 1442.5; DB 10; Length 327;  
 Best Local Similarity 91.2%; Pred. No. 1.6e-127;  
 Matches 289; Conservative 12; Mismatches 15; Indels 1; Gaps 1;

QY 3 LRGTVDPSGFDGRADAEVLRKAMKGLGTDEDSILNLTARSNAQROQIAEEFKTLFGSD 62  
 DB 12 LRGTVDPSGFDGRADAEVLRKAMKGLGTDEDSILNLTARSNAQROQISAAFKTLFGSD 71  
 QY 63 LVNDKSELTKGFEKLIYALMKPSRLYDAYELKAKAGAGTDEKVTETIIASRTPPELRA 122  
 DB 72 LLDLKSSELTKGFEKLIYALMKPSRLYDAYELKAKAGAGTDEKVTETIIASRTPPELRA 131  
 QY 123 IKQAYEEYSGNLEDVVDGTSGYQRMVLLQANRDPDAIDDAQVELDAQALFQAGE 182  
 DB 132 IKQAYEEYSGNLEDVVDGTSGYQRMVLLQANRDPDAIDDAQVELDAQALFQAGE 191  
 QY 183 LKMGDEBEKFTITLGTSSVSHLRVFDKMTISGFQIETIDRETSNLEMLLAUVKSI 242  
 DB 192 LKMGDEBEKFTITLGTSSVSHLRVFDKMTISGFQIETIDRETSNLEMLLAUVKSI 251  
 QY 243 RSIPIAYLAETLYYAMKAGAGTDHDLIRVVSSEIDLFNIRKFRKPFATSLYSMIKSDT 302  
 DB 252 RSIPIAYLAETLYYAMKAGAGTDHDLIRVVSSEIDLFNIRKFRKPFATSLYSMIKSDT 311  
 QY 303 SGDYKXALLLLCGEED 319  
 DB 312 SGDYKXALLLLCGEED 327

RESULT 7  
 US-10-097-340-10

Sequence 10, Application US/10097340  
 Publication No. US20030087250A1  
 GENERAL INFORMATION:  
 APPLICANT: John MONAHAN  
 APPLICANT: Manjula GANNAVARAPU  
 APPLICANT: Sebastian HOERSCHE  
 APPLICANT: Shubhanga KAMATKAR  
 APPLICANT: Steve G. KOVATS

```

APPLICANT: Rachel E. MEYERS
APPLICANT: Michael MORRISSEY
APPLICANT: Peter OLANDT
APPLICANT: Ami SEN
APPLICANT: Peter VEIBY
APPLICANT: Gordon B. MILLS
APPLICANT: Robert C. BAST, Jr.
APPLICANT: Karen LU
APPLICANT: Rosemarie SCHMANDT
APPLICANT: Xunel ZHAO
APPLICANT: Karen GLATT
TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
FILE REFERENCE: MRL-030
CURRENT FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: US/10/097,340
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/276,025
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/325,149
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/276,026
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/324,967
PRIOR FILING DATE: 2001/09/26
PRIOR APPLICATION NUMBER: 60/311,732
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/325,102
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/323,580
PRIOR FILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 363
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 10
LENGTH: 321
TYPE: PRT
ORGANISM: Homo sapiens
US-10-097-340-10

```

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Query Match      57.6%; Score 921; DB 15; Length 321;
Best Local Similarity 57.3%; Pred. No. 2e-78;
Matches 180; Conservative 56; Mismatches 78; Indels 0; Gaps 0;

QY 5 GTVDFSGFDGRADAEVLRKAMKGLGTDESDILNLTARSNARQOIAEFPKTLFGSDLV 64
DB 8 GTVKAASGFNAMEDAQTLRKAMKGLGTDEDAISVLAVRNNAQOEIRTAIXKSTIGRDLI 67
QY 65 NDMKSELTGKFEKLIYALMKPSRLYDAYELKNAKAGAGTDEKVTETIISRTPEELRAIK 124
DB 68 DDKSELISGNFEQVIVGMNTPVLYDVQELRRAMKAGAGTDEGCLIEIISRTPEELIRIS 127
QY 125 QAYEEYSGNLEDDVVGDTSGYVQRMVLVLLQANRPDPTAIDDAQVELDQAALFOAGELK 184
DB 128 QTYOQOYGRSLIEDJRSPTSEMFQVLYSLSAGGRDEBNYIDDLAVRQDQDLVYAGEKK 187
QY 185 WGTDEEKFITLIGTSVSHLRVFDKMTISGFQIETIDRETSIGNENTLLAVKYSIRS 244
DB 188 WGTDEEKFITLIGTSVSHLRVFDKMTISGFQIETIDRETSIGNENTLLAVKYSIRS 247
QY 245 IPAYLAETLYYAMKAGATDHTLIRIVYRSSEIDLFNIRKPKFATSLYSIMIKGPTSG 304
DB 248 KSAVFAEKLYKSNKGLGTDNTLIRVMSRAEIDMDIRAHFKLYGKSLYSFIKGDTS 307
QY 305 DYKVALLLCGGED 318
DB 308 DYKVALLLVCGGDD 321

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RESULT 8
US-09-925-301-1062
Sequence 1062, Application US/09925301
Patent No. US20020052308A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.

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TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1062
LENGTH: 324
TYPE: PRT
ORGANISM: Homo sapiens
US-09-925-301-1062

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```

Query Match      57.6%; Score 921; DB 9; Length 324;
Best Local Similarity 57.3%; Pred. No. 2e-78;
Matches 180; Conservative 56; Mismatches 78; Indels 0; Gaps 0;

QY 5 GTVDFSGFDGRADAEVLRKAMKGLGTDESDILNLTARSNARQOIAEFPKTLFGSDLV 64
DB 11 GTVKAASGFNAMEDAQTLRKAMKGLGTDEDAISVLAVRNNAQOEIRTAIXKSTIGRDLI 70
QY 65 NDMKSELTGKFEKLIYALMKPSRLYDAYELKNAKAGAGTDEKVTETIISRTPEELRAIK 124
DB 71 DDKSELISGNFEQVIVGMNTPVLYDVQELRRAMKAGAGTDEGCLIEIISRTPEELIRIS 130
QY 125 QAYEEYSGNLEDDVVGDTSGYVQRMVLVLLQANRPDPTAIDDAQVELDQAALFOAGELK 184
DB 131 QTYOQOYGRSLIEDJRSPTSEMFQVLYSLSAGGRDEBNYIDDLAVRQDQDLVYAGEKK 190
QY 185 WGTDEEKFITLIGTSVSHLRVFDKMTISGFQIETIDRETSIGNENTLLAVKYSIRS 244
DB 191 WGTDEEKFITLIGTSVSHLRVFDKMTISGFQIETIDRETSIGNENTLLAVKYSIRS 250
QY 245 IPAYLAETLYYAMKAGATDHTLIRIVYRSSEIDLFNIRKPKFATSLYSIMIKGPTSG 304
DB 251 KSAVFAEKLYKSNKGLGTDNTLIRVMSRAEIDMDIRAHFKLYGKSLYSFIKGDTS 310
QY 305 DYKVALLLCGGED 318
DB 311 DYKVALLLVCGGDD 324

```

```

RESULT 9
US-09-925-302-731
Sequence 731, Application US/09925302
Patent No. US20020044941A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA104
CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05918
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 896
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 731
LENGTH: 208
TYPE: PRT
ORGANISM: Homo sapiens
US-09-925-302-731

```

```

Db      8  LRGTVDFFGDFRADAEVLRKAMKGLGTDDESIINLLTARSNAORQOIAEEFKTLFGDRDL 67
QY      63  LVNDKSELTKGEKTIIVALKMPSRLYDAVELKHAKEAGTDEKVTETIISRTPEELRA 122
Db      68  LDDDKSELTKGEKTIIVALKMPSRLYDAVELKHAKEAGTDEKVTETIISRTPEELRA 127
QY      123  IKQAYEEVGSNLEDVVGDTSGYQRMVLVLLQANRDPDTAIDAOVELDAQALFOAGE 182
Db      128  IKQAYEEVGSNLEDVVGDTSGYQRMVLVLLQANRDPDTAIDAOVELDAQALFOAGE 187
QY      183  LKMGDEEKFITITIGTRSV 201
Db      188  LKMGDEEKFITITIGTRSV 206

```

```

RESULT 10
US-10-236-031B-18
; Sequence 18, Application US/10236031B
; Publication No. US20030219760A1
; GENERAL INFORMATION:
; APPLICANT: Gordon, Gavin J.
; APPLICANT: Jensen, Roderick V.
; APPLICANT: Gullans, Steven R.
; APPLICANT: Bueno, Raphael
; TITLE OF INVENTION: Diagnostic and Prognostic Tests
; FILE REFERENCE: B00801/70265 (JRV/JAV)
; CURRENT APPLICATION NUMBER: US/10/236, 031B
; CURRENT FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US 60/317,389
; PRIOR FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/407,431
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-236-031B-18

```

```

Query Match      51.5%; Score 822.5; DB 12; Length 327;
Best Local Similarity 56.8%; Pred. No. 3,9e-69;
Matches 178; Conservative 44; Mismatches 90; Indels 1; Gaps 1;

QY      6  TVTDFSGDFGRADAEVLRKAMKGLGTDDESIINLLTARSNAORQOIAEEFKTLFGDRDL 65
Db      14  TVSSSHFNPDPAETLYKAMKGIQNEQALIDVLRKSNTRQQAISFKAQFOKDLTE 73
QY      66  DMKSELTKGEKTIIVALKMPSRLYDAVELKHAKEAGTDEKVTETIISRTPEELRAIKQ 125
Db      74  TLKSELTKGEKTIIVALKMPSRLYDAVELKHAKEAGTDEKVTETIISRTPEELRAIKQ 133
QY      126  AYESEYGSNLEDVVGDTSGYQRMVLVLLQANRDP-DPAIDAOVELDAQALFOAGELK 184
Db      134  AYESEYGSNLEDVVGDTSGYQRMVLVLLQANRDPVSVFPALADAOQLVNAAGKI 193
QY      185  WGTDEEKFITITIGTRSVSHLRVFDKXMTISGQIETTDRTSGNLENLLIAVYKSTRS 244
Db      194  RGDDEKFIITILCRSTHLLRVFEEYKANKSIDSKSSTHSLSEAMLTAVKCTON 253
QY      245  IPAYIAETLYAMKAGTDHDTLIRIVSRSEIDLPIKREPKNPAATSLYMINIKGDTSG 304
Db      254  LHSYFAERLYAMKAGTDRGTILIRIVSRSEIDLNLKCHKKKYGKTLSEMTVEDTSG 313
QY      305  DYKALLLLCGGE 317
Db      314  DYKALLLLVGS 326

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```

RESULT 11
US-10-316-253-262
; Sequence 262, Application US/10316253
; Publication No. US20030162706A1

```

```

; GENERAL INFORMATION:
; APPLICANT: The Procter & Gamble Company
; APPLICANT: Peters, Kevin
; APPLICANT: Thompson, Larry
; APPLICANT: Wang, Feng
; APPLICANT: Greis, Kenneth
; TITLE OF INVENTION: Angiogenesis Modulating Proteins
; FILE REFERENCE: 8865W
; CURRENT APPLICATION NUMBER: US/10/316, 253
; PRIOR FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: US 60/355,295
; NUMBER OF SEQ ID NOS: 308
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 262
; LENGTH: 324
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-316-253-262

```

```

Query Match      49.2%; Score 787; DB 12; Length 324;
Best Local Similarity 48.6%; Pred. No. 8,5e-66;
Matches 153; Conservative 64; Mismatches 98; Indels 0; Gaps 0;

QY      4  RGTVDFFGDFGRADAEVLRKAMKGLGTDDESIINLLTARSNAORQOIAEEFKTLFGDRDL 63
Db      10  RGTINYPGPNFSDVDAEIRKAIKIGTDEKTLINILTERNAORQIVKHIOAYQAL 69
QY      64  VNDKSELTKGEKTIIVALKMPSRLYDAVELKHAKEAGTDEKVTETIISRTPEELRAI 123
Db      70  KADLKDLISGFHEHVMVALITPAVFDKQKKSNRGWGTDEDTLITRTSRQKKEI 129
QY      124  KQAYEEVGSNLEDVVGDTSGYQRMVLVLLQANRDPDTAIDAOVELDAQALFOAGEL 183
Db      130  SQAYITAYKMLRDDISSSTSDPFRKALLTADGGRBSLKVDHAKKQATLYDAGEK 189
QY      184  KMGDEEKFITITIGTRSVSHLRVFDKXMTISGQIETTDRTSGNLENLLIAVYKSTRS 243
Db      190  KMGDEEKFITITILCRSPFOKLTTFDEYRNISQKDIEDSIKGLSGHFEDLLAVVCTR 249
QY      244  SIPAYIAETLYAMKAGTDHDTLIRIVSRSEIDLPIKREPKNPAATSLYMINIKGDTSG 303
Db      250  NTPAFAGRLHQAAGAGTDETLIRIVSRSEIDLPIRREPKRYGCSLYSAIQSDTS 309
QY      304  GDYKALLLLCGGED 318
Db      310  GDYRTVLLKICGGD 324

```

```

RESULT 12
US-10-205-823-34
; Sequence 34, Application US/10205823
; Publication No. US20030108963A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John B.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavakapu, Manjula
; APPLICANT: Gorbacheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Monsey, Angela M.
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/10/205, 823
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25

```



By	4	RGTVYDPSG	GRDAEVLTKAMKGI	GTDSDILNLLT	TRASNAROOIAEEFK	LTFGRL	63
Best Local Similarity	47.08%	47.08%	47.08%	47.08%	47.08%	47.08%	47.08%
Matches	149	66	97	Indels	0	Gaps	0

DB 265 NKEPDI FAUWLDI DSIKNGNGIKUWLVKIRIMWSKSEVDMKINSEFNKNI GNSLII IVOODIN 327  
QY 304 GDYKALIIICGGED 318  
|||:|||||:|



GenCore version 5.1.6  
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CM protein - protein search, using sw model

Run on: December 12, 2003, 14:47:48 ; Search time 10.6549 Seconds  
(without alignments)  
2879.232 Million cell updates/sec

Title: PCT-US03-24332-3

Perfect score: 1598

Sequence: 1 MALRGVTVPFSGFDGRADAE.....GDTSGDYKALLLCGGEDD 319

Scoring table: BLOSUM62

Searched: 283308 segs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database:

PIR\_76: \*  
1: p1r1: \*  
2: p1r2: \*  
3: p1r3: \*  
4: p1r4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	1585	99.2	1 LUR75	annexin V - rat
2	1467	91.8	2 S27214	annexin V - bovine
3	1451.5	90.8	3 AOHUP	annexin V [validat
4	1257	78.7	4 LUCHS	annexin V - chick
5	934	58.4	5 S52844	annexin VI - rat
6	933	58.4	6 S01786	annexin VI - mouse
7	921	57.6	7 A42077	annexin IV - human
8	919	57.5	8 AOHU68	annexin IV [valida
9	916	57.3	9 LUBO4	annexin IV - bovin
10	915	57.3	10 LUPG4	annexin IV - pig
11	898	56.2	11 JC2029	annexin - chicken
12	876	54.8	12 LURB11	annexin XI - rabbi
13	870	54.4	13 LUBO11	annexin XI form A
14	870	54.4	14 S23447	annexin XI form B
15	858	53.7	15 S05	annexin XI form
16	822.5	51.5	16 A53152	annexin XI - huma
17	792	49.6	17 LURH3	annexin VIII - hum
18	785	49.1	18 LURH3	annexin III - rat
19	763	47.7	19 S29170	annexin III - huma
20	760	47.6	20 LURH3	annexin VII - mus
21	718	44.9	21 LURH12	annexin VII, long
22	695.5	43.5	22 LURH36	annexin XII - Hydr
23	695.5	43.5	23 S33700	annexin II - human
24	692	43.3	24 S41022	annexin II - rat
25	691.5	43.3	25 LUBO36	hypothetical prote
26	688.5	43.1	26 LUMS36	annexin II - bovin
27	688.5	42.8	27 S55277	annexin II - mouse
28	683.5	42.8	28 UQ1298	annexin II - rat
29	682.5	42.7	29 UQ1297	annexin II type 2
				annexin II type 1

30	680.5	42.6	339 1	LUCH2	annexin II - chick
31	676	42.3	512 2	S70644	annexin VII - Afr
32	675	42.2	296 1	LUPF9	annexin IX - fruit
33	673	42.1	316 1	LURH5	annexin XIII, inte
34	671	42.0	321 1	LUPF10	annexin X - fruit
35	665	41.6	316 2	A57076	annexin XIIIa - do
36	665	41.6	357 2	B57076	annexin XIIIb - do
37	652	40.8	346 1	LUGP1	annexin I - guinea
38	626	39.2	346 1	S28228	annexin I - bovine
39	622	38.9	346 1	LURH	annexin I - human
40	620	38.8	343 1	A44118	annexin I type 2 -
41	615	38.5	346 1	LURH1	annexin I - rat
42	613	38.4	346 1	LUMS1	annexin I - mouse
43	596.5	37.3	322 2	B84452	protein ZC15.1 [i
44	570.5	35.7	341 1	LURH1	annexin I type 1 -
45	534.5	33.4	462 1	LUD07	annexin VII - slim

## ALIGNMENTS

### RESULT 1

LUR75

N;Alternate names: endonexin II; lipocortin V; placental anticoagulant protein; place  
N;Species: Rattus norvegicus (Norway rat)  
C;Date: 30-Sep-1992 #sequence\_revision 30-Sep-1992 #text\_change 22-Jun-1999

C;Accession: C29250; S66680

R;Pepinsky, R.B.; Rizard, R.; Metallano, R.J.; Sinclair, L.K.; Miller, G.T.; Brownin

J. Biol. Chem. 263, 10799-10811, 1988

A;Title: Five distinct calcium and phospholipid binding proteins share homology with

A;Reference number: A92659; MUID:88273202; PMID:2968983

A;Accession: C29250

A;Molecule type: mRNA

A;Residues: 1-319 <PEP>

A;Cross-references: GB:M21730; NID:G205138; PID:AAA4512.1; PID:G205139

R;Imai, Y.; Kohsaka, S.

Eur. J. Biochem. 235, 327-334, 1995

A;Title: Structure of rat annexin V gene and molecular diversity of its transcripts.

A;Reference number: S66680; MUID:96035863; PMID:756178

A;Accession: S66680

A;Status: preliminary; translation not shown

A;Molecule type: DNA

A;Cross-references: EMBL:D42136

C;Comment: Annexins undergo reversible, calcium-dependent binding to membrane phospho

deroxid. C;Comment: Annexin V has been proposed to play a role in the inhibition of blood coag

olid-binding rather than proteolytic inactivation. It does not affect thrombin-depe

C;Genetics: 1/3; 30/1; 61/3; 99/3; 130/1; 156/3; 175/3; 207/1; 239/1; 258/3; 299/3

C;Superfamily: annexin I; annexin repeat homology

C;Keywords: calcium binding; duplication; endonexin fold; membrane-associated protein

F;1-319/Product: annexin V #status predicted <MUT>

F;16-87/Domains: annexin repeat homology <X1>

F;27-43/Region: endonexin fold #status predicted

F;88-159/Domains: annexin repeat homology <AX2>

F;99-115/Region: endonexin fold #status predicted

F;171-243/Domains: annexin repeat homology <AX3>

F;183-199/Region: endonexin fold #status predicted

F;247-318/Domains: annexin repeat homology <AX4>

F;258-274/Region: endonexin fold #status predicted

F;325-38-30-70/Binding site: calcium, high affinity (Met, Gly, Glu) #status predi

F;31-33-34/Binding site: calcium, low affinity (Thr, Glu, Asp) #status predicted

F;71-76/Binding site: calcium, low affinity (Leu, Glu) #status predicted

F;98-100-102-142/Binding site: calcium, high affinity (Leu, Gly, Asp) #status pr

F;257-259-261-301/Binding site: calcium, high affinity (Met, Gly, Gly, Asp) #status f

Query Match 99.2% Score 1585; DB 1; Length 319;  
Best local similarity 99.4% Pred. No. 5.1e-96;  
Matches 317; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 MALRGVTVPFSGFDGRADAEVIRKAWKGLGTDDESIINLTLFARNAPQQAIEFFKILFG 60

```

Db      1 MALRTVTDPSGFCORAAEVLKRAMKCLGTDEDSIINLTASNAQROOIAEEFKTLFG 60
QY      61 RDLVNDKMSLTGKFEKLIIVALKMPSRLYDAYELKAKLKGAGDEKYLTIISARFPEEL 120
Db      61 RDLVNDKMSLTGKFEKLIIVALKMPSRLYDAYELKAKLKGAGDEKYLTIISARFPEEL 120
QY      121 RAIKQAYEEYGSNNLEDVVGDTSGYQGRMLVLLQANRPDPAIDDAQVELDAQALFOAGE 180
Db      121 RAIKQAYEEYGSNNLEDVVGDTSGYQGRMLVLLQANRPDPAIDDAQVELDAQALFOAGE 180
QY      181 GELKMGTEDEKFTITLIGRSVSHLRVFDKMTTISGFQIETITDRETSGNLEMLLAVVK 240
Db      181 GELKMGTEDEKFTITLIGRSVSHLRVFDKMTTISGFQIETITDRETSGNLEMLLAVVK 240
QY      241 SIRSIPAYLAETLYYAMKAGAGTDHTLLRVVSSSEIDLVRIRKFRKFNATSLYSMIKG 300
Db      241 SIRSIPAYLAETLYYAMKAGAGTDHTLLRVVSSSEIDLVRIRKFRKFNATSLYSMIKG 300
QY      301 DTSGDYKALLLLCGGEDD 319
Db      301 DTSGDYKALLLLCGGEDD 319

```

## RESULT 2

```

S27214
annexin V - bovine
N:Alternate names: CaBP33; CaBP37
C:Species: Bos primigenius taurus (cattle)
C>Date: 08-Jun-1994 #sequence_revision 10-Feb-1995 #text_change 26-Feb-1999
C:Accession: S27214; S27215
R:Leaumont, M.P.; Howell, S.A.; Harris, A.C.M.; Ames, B.; Patel, Y.; Giambanco, I.; Bi
Biochim. Biophys. Acta 1160, 76-83, 1992
A:Title: Novel isoforms of CaBP 33/37 (Annexin V) from mammalian brain: structural and f
A:Reference number: S27214; MUID:93041974; PMID:1420335
A:Accession: S27214
A:Molecule type: protein
A:Residues: 1-320 <LEA>
A:Accession: S27215
A:Molecule type: protein
A:Residues: 1-35; 'T', 37-124, 'E', 126-320 <LE2>
A:Note: It is uncertain whether the sequence differences are due to allelic variation or
C:Comment: Annexins undergo reversible, calcium-dependent binding to membrane phospholip
C:Comment: Annexin V has been proposed to play a role in the inhibition of blood coagula
O:lipid-binding rather than proteolytic inactivation. It does not affect thrombin-depende
C:Superfamily: annexin I; annexin repeat homology
C:Keywords: acetylated amino end; anticoagulant; calcium binding; duplication; endonexin
F:17-88/Domain: annexin repeat homology <AX1>
F:17-88/Region: endonexin fold #status predicted
F:89-160/Domain: annexin repeat homology <AX2>
F:100-116/Region: endonexin fold #status predicted
F:172-244/Domain: annexin repeat homology <AX3>
F:184-200/Region: endonexin fold #status predicted
F:248-319/Domain: annexin repeat homology <AX4>
F:259-275/Region: endonexin fold #status predicted
F:1/Modified site: acetylated amino end (Ala) #status experimental
F:22/Binding site: phosphate (Thr) (covalent) #status experimental
F:27,29,31,71/Binding site: calcium, high affinity (Met, Gly, Gly, Glu) #status predicte
F:32,34,35/Binding site: calcium, low affinity (Thr, Glu, Glu) #status predicted
F:72,77/Binding site: calcium, low affinity (Leu, Glu) #status predicted
F:99,101,103,143/Binding site: calcium, high affinity (Leu, Gly, Asp) #status predi
F:258,260,262,302/Binding site: calcium, high affinity (Met, Gly, Gly, Asp) #status pred

```

Query Match 91.8%; Score 1467; DB 1; Length 320;

Best local similarity 91.8%; Pred. No. 2,4e-89;

Matches 291; Conservative 10; Mismatches 16; Indels 0; Gaps 0;

```

QY      3 LRGTVTDSGFCORAAEVLKRAMKCLGTDEDSIINLTASNAQROOIAEEFKTLFG 62
Db      4 LRGTVADPFGFPERADAETLRKAMKGLGTDEDSITLTLTSRNSAQROEIAVAFKTLFG 63
QY      63 LVNDKMSLTGKFEKLIIVALKMPSRLYDAYELKAKLKGAGDEKYLTIISARFPEELRA 122

```

```

Db      64 LDDKSELTKGFEKLIIVALKMPSRLYDAYELKAKLKGAGDEKYLTIISARFPEELRA 123
QY      123 IKQAYEEYGSNNLEDVVGDTSGYQGRMLVLLQANRPDPAIDDAQVELDAQALFOAGE 182
Db      124 IKQAYEEYGSNNLEDVVGDTSGYQGRMLVLLQANRPDPAIDDAQVELDAQALFOAGE 183
QY      183 LKMGTEDEKFTITLIGRSVSHLRVFDKMTTISGFQIETITDRETSGNLEMLLAVVKSI 242
Db      184 LKMGTEDEKFTITLIGRSVSHLRVFDKMTTISGFQIETITDRETSGNLEMLLAVVKSI 243
QY      243 RSIPAYLAETLYYAMKAGAGTDHTLLRVVSSSEIDLVRIRKFRKFNATSLYSMIKGT 302
Db      244 RSIPAYLAETLYYAMKAGAGTDHTLLRVVSSSEIDLVRIRKFRKFNATSLYSMIKGT 303
QY      303 SGDYKALLLLCGGEDD 319
Db      304 SGDYKALLLLCGGEDD 320

```

## RESULT 3

ACHUP

annexin V (validated) - human

N:Alternate names: endonexin II; lipocortin V; placental anticoagulant protein; plac

C:Species: Homo sapiens (man)

C>Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 08-Dec-2000

C:Accession: D29250; A30206; A28076; S01016; A29417; A41514; A28038; C31953; S0646;

R:Peplinsky, R.B.; Tizack, R.; Macatallano, R.J.; Sincclair, L.K.; Miller, G.T.; Brown

J. Biol. Chem. 263, 10759-10811, 1988

A:Title: Five distinct calcium and phospholipid binding proteins share homology with

A:Reference number: A28559; MUID:88273202; PMID:2868983

A:Accession: D29250

A:Molecule type: mRNA

A:Residues: 1-320 <PPP>

A:Cross-references: GB:017131; NID:G186969; PIDN:AA53166.1; PID:G307116

R:Grundmann, U.; Abel, K.J.; Bohm, H.; Loebmann, H.; Lottespeltch, F.; Kuepper, H.

Proc. Natl. Acad. Sci. U.S.A. 85, 3708-3712, 1988

A:Title: Characterization of cDNA encoding human placental anticoagulant protein (Pp

A:Reference number: A30206; MUID:8823495; PMID:2867495

A:Accession: A30206

A:Molecule type: mRNA

A:Residues: 1-320 <GRU>

A:Cross-references: GB:M19384; NID:G189614; PIDN:AA55945.1; PID:G189615

R:Kaplan, R.; Jave, M.; Burgess, W.H.; Schlaepfer, D.D.; Haigler, H.T.

J. Biol. Chem. 263, 8037-8043, 1988

A:Title: Cloning and expression of cDNA for human endonexin II, a Ca(2+) and phospho

A:Reference number: A28076; MUID:88228020; PMID:2867291

A:Accession: A28076

A:Molecule type: mRNA

A:Residues: 1-320 <KAP>

A:Cross-references: GB:003745; NID:G182111; PIDN:AA52386.1; PID:G182112

R:Mauner-Fogel, I.; Reutelingersperger, C.P.M.; Pieters, J.; Bodo, G.; Strawowa, C.; Ha

Eit, U. Biochem. 174, 585-592, 1988

A:Title: Cloning and expression of cDNA for human vascular anticoagulant, a Ca-depen

A:Reference number: S01016; MUID:88271329; PMID:2455636

A:Accession: S01016

A:Molecule type: mRNA

A:Residues: 1-320 <MAU>

A:Cross-references: EMBL:X12454; NID:G37636; PIDN:CA30985.1; PID:G37637

A:Note: part of this sequence was confirmed by protein sequencing

R:Funakoshi, T.; Hendrickson, L.S.; McMullen, B.A.; Fujikawa, K.

Biochemistry 26, 8087-8092, 1987

A:Title: Primary structure of human placental anticoagulant protein.

A:Reference number: A29417; MUID:88163463; PMID:2864863

A:Contents: amino-terminal acetylation

A:Accession: A29417

A:Molecule type: mRNA

A:Residues: 1-320 <FUN>

A:Cross-references: EMBL:M18366; NID:G179131; PIDN:AA3570.1; PID:G179132

R:Itawaki, A.; Suda, M.; Nakao, H.; Nagoya, T.; Saito, Y.; Arai, K.; Mizoguchi, T.;

J. Biochem. 102, 1261-1273, 1987

A:Title: Structure and expression of cDNA for an inhibitor of blood coagulation iscl

A:Reference number: A41514; MUID:8819278; PMID:2963810

A:Accession: A41514  
 A:Molecule type: mRNA  
 A:Residues: 1-320 <1WA>  
 A:Cross-references: GB:D00172; NID:g219480; PIDN:BA00122.1; PID:g219481  
 A:Note: part of this sequence was confirmed by protein sequencing  
 R:Schlaepfer, D.D.; Mehlman, T.; Burgess, W.H.; Haigler, H.T.  
 Proc. Natl. Acad. Sci. U.S.A. 84, 6078-6082, 1987  
 A:Title: Structural and functional characterization of endonexin II, a calcium- and phospholipid-binding protein  
 A:Reference number: A28038; PMID:87317598; PMID:2957692  
 A:Accession: A28038  
 A:Molecule type: protein  
 A:Residues: 86-131, 'W', 260-272, 274-297, 300-315, 'X', 317-320 <SCH>  
 R:Ahm, N.G.; Teller, D.C.; Binkowski, M.J.; McMullen, B.A.; Lipkin, E.W.; de Haen, C.  
 J. Biol. Chem. 263, 18657-18663, 1988  
 A:Title: Sedimentation equilibrium analysis of five lipocortin-related phospholipase A-2 isoforms  
 A:Reference number: A92696; PMID:8906652; PMID:2974032  
 A:Accession: C31953  
 A:Molecule type: protein  
 A:Residues: 35-93 <AHN>  
 R:Rohrbaugh, B.; Comer, C.; Cortial, S.; Haumont, P.Y.; Diep Le, K.H.; Cavadore, J.C.; Co Biochem. J. 263, 929-935, 1989  
 A:Title: A 32 kDa lipocortin from human mononuclear cells appears to be identical with lipocortin I  
 A:Reference number: S06646; PMID:90088443; PMID:2532007  
 A:Accession: S06646  
 A:Molecule type: protein  
 A:Residues: 7-25, 27-42, 51-74, 'X', 76-151, 181-198, 202-207, 209-226, 228-238, 246-271, 277-282; R:Huber, R.; Schneider, M.; Mayr, I.; Roemisch, J.; Paques, E.P.  
 FEBS Lett. 275, 15-21, 1990  
 A:Title: The calcium binding sites in human annexin V by crystal structure analysis at 2.0 Å resolution  
 A:Reference number: A37250; PMID:91085549; PMID:2148156  
 A:Contents: annotation; X-ray crystallography, 2.0 angstroms  
 A:Note: three calcium ions are strongly bound at sites in the first, second, and fourth binding site  
 R:Funakoshi, T.; Helmark, R.L.; Hendrickson, L.E.; McMullen, B.A.; Fujikawa, K.  
 Biochemistry 26, 5572-5578, 1987  
 A:Title: Human placental anticoagulant protein: isolation and characterization.  
 A:Reference number: A29670; PMID:88050845; PMID:2960376  
 A:Accession: A29670  
 A:Molecule type: protein  
 A:Residues: 29-73, 1274-297, 300-320 <FUT>  
 R:Fernandez, M.P.; Morgan, R.O.; Fernandez, W.R.; Carcedo, M.T.  
 Gene 148, 253-260, 1994  
 A:Title: The gene encoding human annexin V has a TATA-less promoter with a high G+C content  
 A:Reference number: I37172; PMID:95047484; PMID:7958998  
 A:Accession: I37172  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-320 <RBS>  
 A:Cross-references: EMBL:U01691; NID:g430964; PIDN:AB40047.1; PID:g430966  
 A:Comment: Annexin V has been proposed to play a role in the inhibition of blood coagulation. It does not affect of blood coagulation. It does not affect of blood coagulation. It does not affect of blood coagulation.  
 C:Genetics: GDB:ANX5  
 A:Gene: GDB:ANX5  
 A:Cross-references: GDB:120555; OMIM:131230  
 A:Map position: 4q26-4q28  
 A:Initons: 3/3; 32/1; 63/3; 101/3; 132/1; 158/3; 177/3; 209/1; 241/1; 260/3; 301/3  
 C:Superfamily: annexin I; annexin repeat homolog <AX3>  
 C:Keywords: acetylated amino end; anticoagulant; calcium binding; duplication; endonexin  
 F:1-320/Product: annexin V #status experimental <AXT>  
 F:18-89/Domain: annexin repeat homolog <AX1>  
 F:29-45/Region: endonexin fold #status predicted  
 F:90-161/Domain: annexin repeat homolog <AX2>  
 F:101-117/Region: endonexin fold #status predicted  
 F:173-245/Domain: annexin repeat homolog <AX3>  
 F:185-201/Region: endonexin fold #status predicted  
 F:249-320/Domain: annexin repeat homolog <AX4>  
 F:260-276/Region: endonexin fold #status predicted  
 F:2/Modified site: acetylated amino end (Asp) (in mature form) #status experimental  
 F:23/Binding site: phosphate (Thr) (covalent) #status predicted  
 F:28/30/32/72/Binding site: calcium, high affinity (Met, Gly, Glu) #status experimental  
 F:33/35/36/Binding site: calcium, low affinity (Thr, Glu, Glu) #status experimental

F:73/78/Binding site: calcium, low affinity (Leu, Glu) #status experimental  
 F:100/102/104/144/Binding site: calcium, high affinity (Leu, Gly, Asp) #status experimental  
 F:259/261/263/303/Binding site: calcium, high affinity (Met, Gly, Glu, Asp) #status experimental

Query Match  
 Best Local Similarity 90.8%; Score 1451.5; DB 1; Length 320;  
 Matches 290; Conservative 12; Mismatches 14; Indels 1; Gaps 1;

3 LGATYDPSGPDGRADAEVLRKAMKGLTDEDSILNLTARSAHQOIAEFPKTLFGRD 62  
 5 LGATYDPSGPDGRADAEVLRKAMKGLTDEDSILNLTARSAHQOIAEFPKTLFGRD 64  
 63 LVMDSKSEITGKFEFLITLAKKPSRLDVAIKAKAGAGTDEKVTLEITASRPEELRA 122  
 65 LMDKSEITGKFEFLITLAKKPSRLDVAIKAKAGAGTDEKVTLEITASRPEELRA 124  
 123 IKQAYEEYSGSLTDEVDVGTSGYQRMVLTQANPDPTAIDDAQVLEDAQLFQAGE 182  
 125 IKQAYEEYSGSLTDEVDVGTSGYQRMVLTQANPDPTAIDDAQVLEDAQLFQAGE 184  
 183 LKMGDDEKFTITLTSRVSRLRVPDKMTISGFCIBETIDRETSGNLEMLLAVYKSI 242  
 185 LKMGDDEKFTITLTSRVSRLRVPDKMTISGFCIBETIDRETSGNLEMLLAVYKSI 244  
 243 RSIPAYLAETLYAKKAGAGTDHLLIRIVYRSRSDLFNIRKPKKPAATSLVSMKGD 302  
 245 RSIPAYLAETLYAKKAGAGTDHLLIRIVYRSRSDLFNIRKPKKPAATSLVSMKGD 304  
 303 SGGYKALLILCGEDD 319  
 305 SGGYKALLILCGEDD 320

RESULT 4  
 LUCHS  
 annexin V - chicken  
 N:Alternate names: anchorin CII; endonexin II; lipocortin V; placental anticoagulant I  
 C:Species: Gallus gallus (chicken)  
 C:Date: 30-Sep-1992 #sequence revision 30-Sep-1992 #text\_change 02-Jun-2000  
 A:Accession: A35381; A28623; B40404; S32523; S08771  
 R:Fernandez, M.P.; Selman, O.; Martin, G.R.; Yamada, Y.; Pfeaffle, M.; Deutzmann, R.; J. Biol. Chem. 263, 5921-5925, 1988  
 A:Title: The structure of anchorin CII, a collagen binding protein isolated from chon  
 A:Reference number: A28623; PMID:88186917; PMID:2833522  
 A:Accession: A28623  
 A:Molecule type: mRNA  
 A:Residues: 1-321 <FER>  
 A:Cross-references: GB:M30971; GB:J03194; NID:g211138; PIDN:AAA48591.1; PID:g211139  
 R:Fernandez, M.P.; Selman, O.; Martin, G.R.; Yamada, Y.; Pfeaffle, M.; Deutzmann, R.; J. Biol. Chem. 263, 5921-5925, 1988  
 A:Title: The structure of anchorin CII, a collagen binding protein isolated from chon  
 A:Reference number: A28623; PMID:88186917; PMID:2833522  
 A:Accession: A28623  
 A:Molecule type: mRNA  
 A:Residues: 1-118, 'L', 'K', 'R', 'N', 'R', 'M', 'G', 'E', 'Y', 'A', 'N', 'G', 'R', 'N', 'K', 'T', 'G', 'R', 'R', 'Q', 'A', 'I', 'F', 'R', 'D', 'C', 'W', 'S', 'C', 'C', 'Q', 'I', 'E', 'I', '163-167, 'E', '169-32  
 A:Cross-references: GB:M30971; GB:U03194; NID:g211138  
 R:Fernandez, M.P.; Selman, O.; Martin, G.R.; Yamada, Y.; Pfeaffle, M.; Deutzmann, R.; J. Biol. Chem. 263, 5921-5925, 1988  
 A:Title: The structure of anchorin CII, a collagen binding protein isolated from chon  
 A:Reference number: A28623; PMID:88186917; PMID:2833522  
 A:Accession: A28623  
 A:Molecule type: protein  
 A:Residues: 188-199 <GEN>  
 A:Experimental source: epiphyseal growth plate cartilage (matrix vesicle-enriched mic  
 R:Boustead, C.M.; Brown, R.; Walker, J.H.  
 Biochem. J. 291, 601-608, 1993  
 A:Title: Isolation, characterization and localization of annexin V from chicken liver  
 A:Reference number: S32523; PMID:93249384; PMID:8484740  
 A:Accession: S32523  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 6-20, 85, 'X', 87-88, 'X', 90-93, 'X', 95-96, 'XX', 99-100, 'X', 102-103, 'XX', 106-10  
 C:Comment: Annexins undergo reversible, calcium-dependent binding to membrane phospho



F:449-465/Region: endonexin fold #status predicted  
 F:527-588/Domain: annexin repeat homology <AX7>  
 F:538-554/Region: endonexin fold #status predicted  
 F:602-673/Domain: annexin repeat homology <AX8>  
 F:613-629/Region: endonexin fold #status predicted  
 F:2/Modified site: acetylated amino end (Ala) (in mature form) #status predicted

Query Match 58.4%; Score 933; DB 1; Length 673;  
 Best Local Similarity 57.3%; Pred. No. 3.3e-53;  
 Matches 183; Conservative 53; Mismatches 80; Indels 0; Gaps 0;

QY 4 RGVTFDSGFGDGRADAEVLRKAMKGLGTDSDSTLNLTRSNAPQOIAEEFKTLFGDIL 63  
 DB 11 RGSHTDPDFDADQDAALATAMKFGSGKESLLEITRSKQOELQCSKSLXGDL 70  
 QY 64 VNMKSELTKGFEKLVALMKPSRLDYAVELKAKLAGTDEKVLTEIIASSTPEELPAI 123  
 DB 71 IEDLYELTKGFELLYNLMRPLAYCDAKEIKDAISGIGTDEKCLIEIIASRTNEQMQIL 130  
 QY 124 KOAYEEYGSNLEDDVVGDTSGYGYQSMVLVLLQANRDPDTAIDDAQVELDAQALFOAGEL 183  
 DB 131 VAAVKDAVERDLESDDIGTSGHFGKMLVLLQGTRENDVVSDDLVDQDVLTEAGSL 190  
 QY 184 KMGTDSEKFTITIGTSVSHLRVPKXWTISGFOIEETIDETSQNLLENLLAVKSIK 243  
 DB 191 KMGTFDAQFIYILGNRSKQHLRVEDEYLTGKPIEASIRGELSGDFKMLAVKICIR 250  
 QY 244 SIPLVLAETLYAMKAGTDDHLLIVYSRSIDLFNIRKFRKRFASLYSMKGTIS 303  
 DB 251 STEPLFAERLPFKAMKGLGTDNLTIRIWSRSELDMDIREIFRTYKSLYSMTKNDTS 310  
 QY 304 GDYKKALLLGGEDD 319  
 DB 311 GEYKKALLKCGGDD 326

## RESULT 7

A:42077  
 N:Annexin IV - human

A:Alternate names: endonexin I, placental anticoagulant protein II; PP4-X protein

C:Species: Homo sapiens (man)

C:Date: 30-Jan-1993 #sequence revision 26-May-1994 #text\_change 22-Jun-1999

C:Accession: A42077; B42077; S07434; A11953; A31046

R:Alt, J.E., Smith, C., Frankenderry, D.A.; Miao, C.H.; Adler, D.A.; Distche, C.M.

Genomics 12, 313-318, 1992

A:Title: Chromosomal mapping of the human annexin IV (ANX4) gene.

A:Reference number: A42077; PMID:92155721; PMID:1346776

A:Accession: A42077

A:Molecule type: mRNA

A:Residues: 1-321 <TAI>

A:Cross-References: GB:M82809; NID:G178698; PIND:AA51740.1; PID:G178699

A:Accession: B42077

A:Molecule type: DNA

A:Residues: 87-129 <TA2>

A:Grundmann, U.; Amann, E.; Kuemper, H.A.

A:Title: Isolation and expression of cDNA coding for a new member of the phospholipase A

A:Reference number: S07434; PMID:8309022; PMID:2970257

A:Accession: S07434

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-97, 'Q', 99-321 <GRU>

A:Cross-References: EMBL:M9383; NID:G189616; PIND:AA041689.1; PID:G189617

R:Ahm, N.G.; Teller, D.C.; Bielekowsky, M.J.; McMullen, B.A.; Lipkin, E.W.; de Haen, C.

J. Biol. Chem. 265, 18657-18663, 1988

A:Title: Sedimentation equilibrium analysis of five lipocortin-related phospholipase A-2

A:Reference number: A92696; PMID:8906652; PMID:2974032

A:Accession: A31953

A:Molecule type: protein

A:Residues: 29-58,101-126,282-310 <ARN>

R:Alt, J.E.; Sakata, M.; McMullen, B.A.; Miao, C.H.; Funakoshi, T.; Hendrickson, L.E.;

Biochemistry 27, 6268-6276, 1988

A:Title: Placental anticoagulant proteins: isolation and comparative characterization

A:Reference number: A90534; PMID:89118212; PMID:2975506

A:Accession: A31046

A:Molecule type: protein

A:Residues: 4-17,30-74,102-146,283-321 <TA3>

C:Genes:

A:Gene: GDB:ANX4

A:Cross-References: GDB:131395; OMTM:106491

A:Map position: 2p13-2p13

A:Insertions: 102/3

C:Superfamily: annexin I; annexin repeat homology

F:2-321/Product: annexin IV #status predicted <AAT>

F:2-321/Domain: annexin repeat homology <AX1>

F:30-46/Region: endonexin fold #status predicted

F:91-162/Domain: endonexin repeat homology <AX2>

F:102-118/Region: endonexin fold #status predicted

F:174-246/Domain: endonexin repeat homology <AX3>

F:186-202/Region: endonexin fold #status predicted

F:250-321/Domain: endonexin repeat homology <AX4>

F:261-277/Region: endonexin fold #status predicted

F:2/Modified site: acetylated amino end (Ala) (in mature form) #status predicted

F:9/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

F:247/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 57.6%; Score 921; DB 1; Length 321;  
 Best Local Similarity 57.3%; Pred. No. 8e-53;  
 Matches 180; Conservative 56; Mismatches 78; Indels 0; Gaps 0;

QY 5 GIVTFDSGFGDGRADAEVLRKAMKGLGTDSDSTLNLTRSNAPQOIAEEFKTLFGDILV 64  
 DB 8 GTVKAASGPNAMEDAQTRKAMKGLGTDSDSTLNLTRSNAPQOIAEEFKTLFGDILV 67  
 QY 65 NVMKSELTKGFEKLVALMKPSRLDYAVELKAKLAGTDEKVLTEIIASSTPEELPAIK 124  
 DB 68 DDKLSLSNFEQVIVGMFTVLYVOELRRANKAGTDEKCLIEIIASSTPEELPAIK 127  
 QY 125 QAYEEYGSNLEDDVVGDTSGYGYQSMVLVLLQANRDPDTAIDDAQVELDAQALFOAGELK 184  
 DB 128 QTVQOQYGRSLDDIRSDTSFMFQVIVLSANGRDEENYDLDLVQDQDVLTEAGELK 187  
 QY 185 KMGTDSEKFTITIGTSVSHLRVPKXWTISGFOIEETIDETSQNLLENLLAVKSIK 244  
 DB 188 KMGTFDAQFIYILGNRSKQHLRVEDEYLTGKPIEASIRGELSGDFKMLAVKICIR 247  
 QY 244 SIPLVLAETLYAMKAGTDDHLLIVYSRSIDLFNIRKFRKRFASLYSMKGTIS 304  
 DB 248 KSAVFAERLPFKAMKGLGTDNLTIRIWSRSELDMDIREIFRTYKSLYSMTKNDTS 307  
 QY 305 DYKKALLLGGEDD 318  
 DB 308 DYRKALLVLCGGDD 321

## RESULT 8

A:Q8H68  
 N:Annexin VI [validated] - human

A:Alternate names: calcium-binding protein, 68k, calelectrin, calphobindin II

C:Species: Homo sapiens (man)

C:Date: 31-Mar-1992 #sequence revision 30-Sep-1992 #text\_change 08-Dec-2000

C:Accession: J00032; S00263; S18519; A31079; JX0091; B34459; B31953; A33507

R:Wasaiki, A.; Suda, M.; Watanabe, M.; Naka, H.; Hattori, Y.; Nagoya, T.; Sano, Y.;

J. Biochem. 106, 43-49, 1989

A:Title: Structure and expression of cDNA for calphobindin II, a human placental coag

A:Reference number: J00032; PMID:89380132; PMID:2528541

A:Accession: J00032

A:Molecule type: mRNA

A:Residues: 1-673 <TWA>

A:Cross-References: EMBL:U00510; NID:Q219550; PIND:BA00400.1; PID:Q219551

R:Crompton, M.R.; Owens, R.J.; Totcy, N.F.; Mose, S.E.; Waterfield, M.D.; Crompton, M

EMBO J. 7, 21-27, 1988

A:Title: Primary structure of the human, membrane-associated Ca(2+)-binding protein p

A:Reference number: S00263; PMID:85196081; PMID:3258820



A/Molecule type: mRNA  
 A/Residues: 1-618, 'D', 620-673 <CR1>  
 A/Cross-references: EMBL:Y000097; NID:935217; PIDN:CAA68286.1; PID:935218  
 A/Accession: S18519  
 A/Molecule type: protein  
 A/Residues: 103-113;167-172, 'X', 174-177;232-235, 'F', 237-240;251-258;277-281;359-362, 'G',  
 A/Note: the sequence from Fig. 6 is inconsistent with that from Fig. 4 in having 619-Glu  
 A/Note: eight calcium ions are bound in the presence of phospholipid  
 R/Suedoc, I.C.; Staughter, C.A.; Jeznick, I.; Barton, P.; Reynolds, G.A.  
 Proc. Natl. Acad. Sci. U.S.A. 85, 664-668, 1988  
 A/Title: Human 67-kDa calelectrin contains a duplication of four repeats found in 35-kDa  
 A/Reference number: A31079; MUID:88124902; PMID:2963335  
 A/Accession: A31079  
 A/Molecule type: mRNA  
 A/Residues: 1-225, 'MK', 228-554, 'T', 556-672 <SUE>  
 A/Cross-references: GB:J03578; NID:917975; PIDN:AAA35656.1; PID:917976  
 R/Yoshizaki, H.; Mizoguchi, T.; Arai, K.; Shiratsuchi, M.; Shidara, Y.; Maki, M.  
 J. Biochem. 107, 43-50, 1990  
 A/Title: Structure and properties of calphobindin II, an anticoagulant protein from huma  
 A/Reference number: JX0091; MUID:90236978; PMID:2139657  
 A/Accession: JX0091  
 A/Molecule type: protein  
 A/Residues: 2-289;307-314;320-445;447-549;581-673 <YOS>  
 R/Hayashi, H.; Owada, M.K.; Sonobe, S.; Kakunaga, T.  
 J. Biol. Chem. 264, 17222-17230, 1989  
 A/Title: Characterizations of two distinct Ca(2+)-dependent phospholipid-binding protein  
 A/Reference number: A34459; MUID:90008880; PMID:2529258  
 A/Accession: B34459  
 A/Molecule type: protein  
 A/Residues: 10-25;69-75;136-151;192-207;209-220;300-306 <HAY>  
 A/Experimental source: placenta  
 R/Bhm, N.G.; Teller, D.C.; Blenowski, M.J.; McMullen, B.A.; Lipkin, E.W.; de Haen, C.  
 J. Biol. Chem. 263, 18657-18663, 1988  
 A/Title: Sedimentation equilibrium analysis of five lipocortin-related phospholipase A-2  
 A/Reference number: A92696; MUID:8906652; PMID:2974032  
 A/Accession: B31953  
 A/Molecule type: protein  
 A/Residues: 90-108, 'L', 110-126;127, 265-276;286-302;626-654 <AHN>  
 R/Hyatt, S.L.; Liao, L.; Chapline, C.; Jaken, S.  
 Biochemistry 33, 1223-1228, 1994  
 A/Title: Identification and characterization of alpha-protein kinase C binding proteins  
 A/Reference number: A53507; MUID:94153907; PMID:8110754  
 A/Accession: A53507  
 A/Molecule type: protein  
 A/Residues: 'X', 473-480, 'DY' <HYA>  
 A/Comment: This abundant cytosolic protein binds to the inner surface of the cell membra  
 C/Genetics:  
 A/Genes: GDB:ANX6  
 A/Cross-references: GDB:119681; OMIM:114070  
 A/Map position: 5q32-5q34  
 C/Superfamily: annexin VI; annexin repeat homology  
 C/Keywords: acetylated amino end; calcium binding; duplication; endonexin fold; phosphol  
 F/2-673/Domain: annexin VI #status experimental <MAY>  
 F/23-94/Domain: annexin repeat homology <AX1>  
 F/34-50/Region: endonexin fold #status predicted  
 F/35-166/Domain: annexin repeat homology <AX2>  
 F/106-122/Region: endonexin fold #status predicted  
 F/178-250/Domain: annexin repeat homology <AX3>  
 F/190-206/Region: endonexin fold #status predicted  
 F/254-325/Domain: annexin repeat homology <AX4>  
 F/265-281/Region: endonexin fold #status predicted  
 F/366-437/Domain: annexin repeat homology <AX5>  
 F/377-393/Region: endonexin fold #status predicted  
 F/438-509/Domain: annexin repeat homology <AX6>  
 F/449-465/Region: endonexin fold #status predicted  
 F/527-598/Domain: annexin repeat homology <AX7>  
 F/538-554/Region: endonexin fold #status predicted  
 F/602-673/Domain: annexin repeat homology <AX8>  
 F/613-629/Region: endonexin fold #status predicted  
 F/2/Modified site: acetylated amino end (Ala) (in mature form) #status experimental

Query Match 57.5%; Score 919; DB 1; Length 673;  
 Best Local Similarity 56.3%; Pred. No. 2,7e-52;  
 Matches 178; Conservative 58; Mismatches 80; Indels 0; Gaps 0;  
 QY 4 RGVTPSGPGRADAEVLRKMKGLGTDEBILNLTLRSNAQRCQIAEEFKTLFGRL 63  
 DB 11 RGSIHDPGRDPDQADALVYANKGFGSKENILDLITRSRQROEVQGSYKSLYKMDL 70  
 QY 64 VMDKSLTLKFEKILVAMKPSRLYDAVELKAKLGAQTDKVLTEIIASTPEELAI 123  
 DB 71 IADKYLTKFPERLLVGNRRPAYCAKEIKDAISGTDKCEIEIASRTNQMQQL 130  
 QY 124 KOAEEFGNLTEDVDVGTSGYQMLVYLQANRPDPTAIDDAQVELEDAQALFOAGEL 183  
 DB 131 VAAKMDAYEDLEADIIIDTSSGFQMLVLLQGTREDDVSEDLVQDDLYEAGEL 190  
 QY 184 KMGTDSEKFTITIGTSVSHLRVPFKYTWISGFQIEITDETSNLEMLLAVYKSR 243  
 DB 191 KMGDEAKQFTYIIGNSKQHLRLVPEYIKTKPEIASIRGELSGDFEXMLAVVKIR 250  
 QY 244 SIPAYLAETLYAMKAGTDGDTLIRVYSRSEIDLFNIRKPEFRKNFATSLYSMTKQTS 303  
 DB 251 STPEYFAERLPKMKGLGTDLNLTIRMSRSELDMDIRBIFRKYKSLYSMTKQTS 310  
 QY 304 GDYKXALLDQGEED 319  
 DB 311 GEYKTLTKLSGGDD 326  
 RESULT 9  
 LUBO4  
 N/Alternate names: 33k calelectrin; chromobindin IV; endonexin; lipocortin IV; prote  
 C/Species: Bos primigenius taurus (cattle)  
 C/Date: 30-Sep-1992 #sequence revision 30-Sep-1992 #ext change 22-Jun-1999  
 R/Accession: A31578; D45066; S59624; A45066; B45066; C45066; F45066; H45066  
 R/Hatman, H.C.; Galfrey, L.C.; Lynch, K.R.; Creutz, C.E.  
 Biochem. Biophys. Res. Commun. 156, 660-667, 1988  
 A/Title: Cloning and characterization of a cDNA encoding bovine endonexin (chromobin  
 A/Reference number: A31578; MUID:89050088; PMID:2847715  
 A/Accession: A31578  
 A/Molecule type: mRNA  
 A/Residues: 1-319 <HAM>  
 A/Cross-references: GB:A13627; NID:9215; PIDN:CAA1954.1; PID:9215; GB:M22248; NID:9  
 R/Kojima, K.; Ogawa, H.K.; Sano, N.; Yamamoto, K.; Irimura, T.; Osawa, T.; Matsumoto  
 J. Biol. Chem. 267, 20536-20539, 1992  
 A/Title: Carbohydrate-binding proteins in bovine kidney have consensus amino acid seq  
 A/Reference number: A45066; MUID:93015942; PMID:1400371  
 A/Accession: D45066  
 A/Molecule type: protein  
 A/Residues: 10-18, 'X', 20-22, 'X', 24-25;29-48;101-107, 'X', 109-118, 'X', 194-197, 'Y', 199,  
 A/Experimental source: kidney  
 A/Note: these fragments are derived from a 33k protein that exhibited Ca++-dependent  
 A/Note: 12-Met and 12-Tyr were also found  
 R/Sohna, H.; Matsushima, N.; Matanabe, T.; Hattori, A.; Kuroki, Y.; Akino, T.  
 Biochem. J. 312, 175-181, 1995  
 A/Title: Ca(2+)-dependent binding of annexin IV to surfactant protein A and lamellar  
 A/Reference number: S59624; MUID:96077142; PMID:7492310  
 A/Accession: S59624  
 A/Status: Preliminary  
 A/Molecule type: protein  
 A/Residues: 29-44;72-77;112-119;163-180;181-190;226-235 <SOH>  
 C/Comment: Annexins undergo reversible, calcium-dependent binding to membrane phosph  
 C/Superfamily: annexin I; annexin repeat homology  
 C/Keywords: calcium binding; duplication; endonexin fold; glycoprotein; phospholipid  
 F/2-319/Product: annexin IV #status predicted <MAY>  
 F/17-88/Domain: annexin repeat homology <AX1>  
 F/128-44/Region: endonexin fold #status predicted  
 F/89-160/Domain: annexin repeat homology <AX2>  
 F/100-116/Region: endonexin fold #status predicted  
 F/172-244/Domain: annexin repeat homology <AX3>



F:184-200/Region: endonexin fold #status predicted  
 F:248-319/Domain: annexin repeat homology <AX4>  
 F:259-275/Region: endonexin fold #status predicted  
 F:7/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted  
 F:125/245/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 57.3%; Score 9.6; DB 1; Length 319;  
 Best Local Similarity 57.3%; Pred. No. 1.7e-52;  
 Matches 180; Conservative 54; Mismatches 80; Indels 0; Gaps 0;

QY 5 GTVTDFSGFDGRDAEVLKRAKMGKGTDESDTLNLTARNSAQRQIAEERKTLFGRLV 64  
 DB 6 GTVKAASGFMAEDQATLRKAMKGLGTDEDAIINTLAYRSTQGEIRAYKTTIGRDL 65  
 QY 65 NDKMSLTKGKEKTLVAMKPSRLYDAVELKAKLGAGDEKVLTEIIASRPEELPAIK 124  
 DB 66 DDUKSELNAGFEVILGMMTPVLVDVQELKRAKMGAGTDEGCLLEIIASRPEELIRIN 125  
 QY 125 QAYEEYGSNLEDVVDGTSYGYQRMVLVLLQANRDPDAIDDAQVELDAQALFOAGELK 184  
 DB 126 QTVQCYGRSLIEDDIRSTISFMFORVLVLSAGRDESNVLDALMRQADQDLYEAGEK 185  
 QY 185 WGTDEKRTITLIGRSVSHLRVFDKRYMTISGFOEETIDRETSGNLENTLLAVKSI 244  
 DB 186 WGTDEVKFLTVLCSNRNHLHFDEYKRIAQDIEQSIKSTSGSFEDALLAVKCMRN 245  
 QY 245 IPAYLAETLYYAMKAGTDHTLIRIVSSEIDLFNIRKEPRKFAISLXSMIKGDTSG 304  
 DB 246 KSAIFYAEKLYKSMKGLGTDDTLIRVVSRAEIMDMDIRANKRLYKSLYSFIKGDTS 305  
 QY 305 DYKXALLILCGED 318  
 DB 306 DYKXVLLILCGDD 319

## RESULT 10

LUP64  
 N:Annexin IV - pig  
 N:Alternate names: 32K callectrin; chromobindin IV; endonexin; lipocortin IV; protein I  
 C:Species: Sus scrofa domestica (domestic pig)  
 C:Date: 30-Sep-1992 #sequence\_revision 30-Sep-1992 #text\_change 24-Nov-1999  
 C:Accession: A27107  
 R:Weber, K.; Johansson, N.; Plessmann, U.; Van, P.N.; Soling, H.D.; Ampe, C.; Vandekerckh  
 EMBL J. 6 1599-1604, 1987  
 A:Title: The amino acid sequence of protein II and its phosphorylation site for protein  
 A:Reference number: A27107; MUID:87275850; PMID:2956093  
 A:Accession: A27107  
 A:Molecule type: protein  
 A:Residues: 1-318 <WEB>  
 A:Experimental source: intestinal epithelium  
 C:Comment: Annexins undergo reversible, calcium-dependent binding to membrane phospholip  
 deretocod.

C:Superfamily: annexin I; annexin repeat homology  
 C:Keywords: blocked amino end; calcium binding; duplication; endonexin fold; glycoprotein  
 F:16-87/Domain: annexin repeat homology <AX1>  
 F:27-43/Region: endonexin fold #status predicted  
 F:88-159/Domain: annexin repeat homology <AX2>  
 F:99-115/Region: endonexin fold #status predicted  
 F:111-243/Domain: annexin repeat homology <AX3>  
 F:163-199/Region: endonexin fold #status predicted  
 F:247-318/Domain: annexin repeat homology <AX4>  
 F:248-274/Region: endonexin fold #status predicted  
 F:1/Modified site: phosphate (Thr) (covalent) (by protein kinase C) #status experimental  
 F:6/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted  
 F:124/244/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 57.3%; Score 9.15; DB 1; Length 318;

Best Local Similarity 57.3%; Pred. No. 1.9e-52;  
 Matches 180; Conservative 55; Mismatches 79; Indels 0; Gaps 0;

QY 5 GTVTDFSGFDGRDAEVLKRAKMGKGTDESDTLNLTARNSAQRQIAEERKTLFGRLV 64  
 DB 5 GTVKAASGFMAEDQATLRKAMKGLGTDEDAIINTLAYRSTQGEIRAYKTTIGRDL 64

QY 65 NDKMSLTKGKEKTLVAMKPSRLYDAVELKAKLGAGDEKVLTEIIASRPEELPAIK 124  
 DB 65 DDUKSELNAGFEVILGMMTPVLVDVQELKRAKMGAGTDEGCLLEIIASRPEELIRIN 124  
 QY 125 QAYEEYGSNLEDVVDGTSYGYQRMVLVLLQANRDPDAIDDAQVELDAQALFOAGELK 184  
 DB 126 QTVQCYGRSLIEDDIRSTISFMFORVLVLSAGRDESNVLDALMRQADQDLYEAGEK 185  
 QY 185 WGTDEKRTITLIGRSVSHLRVFDKRYMTISGFOEETIDRETSGNLENTLLAVKSI 244  
 DB 186 WGTDEVKFLTVLCSNRNHLHFDEYKRIAQDIEQSIKSTSGSFEDALLAVKCMRN 244  
 QY 245 IPAYLAETLYYAMKAGTDHTLIRIVSSEIDLFNIRKEPRKFAISLXSMIKGDTSG 304  
 DB 246 KSAIFYAEKLYKSMKGLGTDDTLIRVVSRAEIMDMDIRANKRLYKSLYSFIKGDTS 304  
 QY 305 DYKXALLILCGED 318  
 DB 306 DYKXVLLILCGDD 319

## RESULT 11

JC2029  
 N:Annexin - chicken  
 N:Alternate names: 67K lipid-dependent Ca2+-binding protein  
 C:Species: Gallus gallus (chicken)  
 C:Date: 30-Sep-1993 #sequence\_revision 20-Aug-1994 #text\_change 17-Mar-1999  
 C:Accession: JC2029  
 R:Caio, X.; Genge, B.R.; Wu, L.N.Y.; Buzzl, W.R.; Showman, R.M.; Wuthier, R.E.  
 Biochem. Biophys. Res. Commun. 197, 556-561, 1993  
 A:Title: Characterization, cloning and expression of the 67-kDa annexin from chicken  
 A:Reference number: JC2029; MUID:94092130; PMID:8267550  
 A:Accession: JC2029  
 A:Molecule type: mRNA  
 A:Residues: 1-671 <CAO>  
 C:Superfamily: annexin VI; annexin repeat homology  
 C:Keywords: calcium binding; phospholipid binding  
 F:21-92/Domain: annexin repeat homology <AX1>  
 F:93-164/Domain: annexin repeat homology <AX2>  
 F:176-248/Domain: annexin repeat homology <AX3>  
 F:252-323/Domain: annexin repeat homology <AX4>  
 F:364-435/Domain: annexin repeat homology <AX5>  
 F:436-507/Domain: annexin repeat homology <AX6>  
 F:525-597/Domain: annexin repeat homology <AX7>  
 F:601-671/Domain: annexin repeat homology <AX8>

Query Match 56.2%; Score 8.98; DB 2; Length 671;  
 Best Local Similarity 57.0%; Pred. No. 6.3e-51;  
 Matches 180; Conservative 54; Mismatches 82; Indels 0; Gaps 0;

QY 4 RGTVTDFSGFDGRDAEVLKRAKMGKGTDESDTLNLTARNSAQRQIAEERKTLFGRLV 63  
 DB 9 RGSVDFPQFNASQADALCNAMKGFSGDKAIIIDLTIRSNKQRLICAYXSQYKDL 68  
 QY 64 VNDKMSLTKGKEKTLVAMKPSRLYDAVELKAKLGAGDEKVLTEIIASRPEELPAIK 123  
 DB 63 IADIKELTKGERKRLIVSLMPPRAYSDAKELKDAIAGIGDEKLIILASRTNGEHL 128  
 QY 124 QAYEEYGSNLEDVVDGTSYGYQRMVLVLLQANRDPDAIDDAQVELDAQALFOAGEL 183  
 DB 123 VAAVDAERDLEADVVDGTSYGYQRMVLVLLQANRDPDAIDDAQVELDAQALFOAGEL 186  
 QY 184 KNGTDEKRTITLIGRSVSHLRVFDKRYMTISGFOEETIDRETSGNLENTLLAVKSI 243  
 DB 183 KNGTDEKRTITLIGRSVSHLRVFDKRYMTISGFOEETIDRETSGNLENTLLAVKSI 246  
 QY 244 SIPAYLAETLYYAMKAGTDHTLIRIVSSEIDLFNIRKEPRKFAISLXSMIKGDTSG 303  
 DB 249 STAFYAEKLYKAMKGLGTDDTLIRVVSRAEIMDMDIRANKRLYKSLYSFIKGDTS 308  
 QY 304 DYKXALLILCGED 319

Db 309 GEYKALLKCEGDD 324

# RESULT 12

LURE11

annexin XI - rabbit

N/Alternate names: calyculin-associated annexin protein CAP-50

C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text\_change 16-Jun-2000

C/Accession: J06094, F0950, A38250, P60263

R/Tokumitsu, H.; Mizutani, A.; Muramatsu, N.; Yokota, T.; Arai, K.; Hidaka, H.

Biochem. Biophys. Res. Commun. 186, 1227-1235, 1992

A/Title: Molecular cloning of rabbit CAP-50, a calyculin-associated annexin protein.

A/Reference number: J06094; MUID:92378579; PMID:1380798

A/Accession: J06094

A/Molecule type: mRNA

A/Residues: 1-503 <TOW>

A/Cross-references: DBJ:U0883; NID:9471147; PID:BA01705.1; PID:9471148

A/Experimental source: lung

A/Accession: P09050

A/Molecule type: protein

A/Residues: 104-141/213-223, 'X', 225-231/254-263/270-280/285-309/319-337/429-448/478-492 <TK2>

R/Tokumitsu, H.; Mizutani, A.; Minami, H.; Kobayashi, R.; Hidaka, H.

J. Biol. Chem. 267, 8919-8924, 1992

A/Title: A calyculin-associated protein is a newly identified member of the Ca(2+)/phospho

A/Reference number: A38250; MUID:92250478; PMID:1533622

A/Accession: A38250

A/Molecule type: protein

A/Residues: 104-141/213-223, 'X', 225-231/254-263/270-280/285-291, 'X', 293-300, 'X', 302-309,

C/Comment: This protein binds specifically to calyculin in a Ca2+ dependent manner.

C/Keywords: calcium binding; annexin repeat homology

C/Keywords: calcium binding; duplication; endonexin fold; glycoprotein; phospholipid bin

F/201-272/Domain: annexin repeat homology <AX1>

F/212-228/Region: endonexin fold #status predicted

F/273-344/Domain: annexin repeat homology <AX2>

F/284-300/Region: endonexin fold #status predicted

F/356-428/Domain: annexin repeat homology <AX3>

F/368-384/Region: endonexin fold #status predicted

F/432-503/Domain: annexin repeat homology <AX4>

F/443-459/Region: endonexin fold #status predicted

F/58/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 54.8%; Score 876; DB 1; Length 503;  
Best Local Similarity 55.6%; Pred. No. 1,2e-49;  
Matches 175; Conservative 56; Mismatches 84; Indels 0; Gaps 0;

4 RGVTFSGFGDADAEVLRKMGKGTDEDSINILTPARSAQROQIAEEFKTLFGRL 63

189 RGTITDASGFDPLRDAEVLRAKMGKGTDEQAIIDCLGSRKQROQLLSFKRAYGDL 248

64 VDMKSELTGKPEKILVALMKPSRLYDAVELKHAAGTDEKVLTEIIASRTPEELRAI 123

249 IKDLKSELGNFEKTLILMKTPILFPAVEIKKAKAGTDEACILFIASRNEHIREL 308

124 KQAYEEYGSNLEDVVGDTSGYQRMVLVLLQANRDPDAIDDAQVELDAQALFQAGEL 183

309 NRAYKTEPKTLEAIRSDTSGHFORLLISQNRDESNVMSLVQEDVQELVYAAGIN 368

184 KMGDEKFTIILGTRSVSHLRVPDKYMTISGQIETIDRETSGLLELLAVYKSI 243

369 FLGTDESKFNVALCSRAHLVAVFNEYQRTGDIKSIKREWSGLDEGMALVAVCKL 428

244 SIPAYLAETLYYAMKAGTDHTLIRIVSRSEIDLFINRKEFRKFNATSLYMKIGDT 303

429 NTPAFPAERLNKAKMGAGTDRTLIRIVSRSEIDLDIRAYEKYKSLYHDITGDT 488

304 GDYKALLLCCGED 318

489 GDYKILLKTCGGND 503

Db 489 GDYKILLKTCGGND 503

## RESULT 13

LURE11

annexin XI form A - bovine

N/Alternate names: calyculin-associated protein peptide, CAP-50

C/Species: Bos primigenius taurus (cattle) #sequence revision 31-Mar-1993 #text\_change 22-Jun-1999

C/Date: 31-Mar-1993 #sequence revision 31-Mar-1993 #text\_change 22-Jun-1999

C/Accession: A42113; A42909; B42909; C42909; D42909

R/Towle, C.A.; Treadwell, B.V.

J. Biol. Chem. 267, 5416-5423, 1992

A/Title: Identification of a novel mammalian annexin. cDNA cloning, sequence analysis

A/Reference number: A42113; MUID:92184796; PMID:1372001

A/Accession: A42113

A/Molecule type: mRNA

A/Residues: 1-503 <TOW>

A/Cross-references: GB:M82802; NID:9162673; PID:AAA0379.1; PID:9162674

A/Note: the authors did not translate the codon GAC for residue 503

R/Mizutani, A.; Usuda, N.; Tokumitsu, H.; Minami, H.; Yasui, K.; Kobayashi, R.; Hidaka

J. Biol. Chem. 267, 13498-13504, 1992

A/Title: CAP-50, a newly identified annexin, localizes in nuclei of cultured fibroblasts

A/Reference number: A42909; MUID:92317074; PMID:1618851

A/Accession: A42909

A/Molecule type: protein

A/Residues: 213-223, 'X', 225-226/319-325, 'G', 327-328, 'X', 330-333, 'Q', 335-339/441-450, 'A'

A/Experimental source: lung

A/Note: sequence modified after extraction from NCBI backbone

C/Comment: Annexins undergo reversible, calcium-dependent binding to membrane phospho

lipids.

C/Genetics:

A/Introns: 19/1; 56/2

A/Note: the list of introns is incomplete

C/Superfamily: annexin VII; annexin repeat homology

C/Keywords: calcium binding; duplication; endonexin fold; glycoprotein; phospholipid

F/201-272/Domain: annexin repeat homology <AX1>

F/212-228/Region: endonexin fold #status predicted

F/273-344/Domain: annexin repeat homology <AX2>

F/284-300/Region: endonexin fold #status predicted

F/356-428/Domain: annexin repeat homology <AX3>

F/368-384/Region: endonexin fold #status predicted

F/443-459/Region: endonexin repeat homology <AX4>

F/443-459/Region: endonexin fold #status predicted

F/59/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 54.4%; Score 870; DB 1; Length 503;  
Best Local Similarity 55.6%; Pred. No. 2.9e-49;  
Matches 175; Conservative 54; Mismatches 86; Indels 0; Gaps 0;

4 RGVTFSGFGDADAEVLRKMGKGTDEDSINILTPARSAQROQIAEEFKTLFGRL 63

189 RGTITDASGFDPLRDAEVLRAKMGKGTDEQAIIDCLGSRKQROQLLSFKRAYGDL 248

64 VDMKSELTGKPEKILVALMKPSRLYDAVELKHAAGTDEKVLTEIIASRTPEELRAI 123

249 IKDLKSELGNFEKTLILMKTPILFPAVEIKKAKAGTDEACILFIASRNEHIREL 308

124 KQAYEEYGSNLEDVVGDTSGYQRMVLVLLQANRDPDAIDDAQVELDAQALFQAGEL 183

309 NRAYKTEPKTLEAIRSDTSGHFORLLISQNRDESNVMSLVQEDVQELVYAAGIN 368

184 KMGDEKFTIILGTRSVSHLRVPDKYMTISGQIETIDRETSGLLELLAVYKSI 243

369 FLGTDESKFNVALCSRAHLVAVFNEYQRTGDIKSIKREWSGLDEGMALVAVCKL 428

244 SIPAYLAETLYYAMKAGTDHTLIRIVSRSEIDLFINRKEFRKFNATSLYMKIGDT 303

429 NTPAFPAERLNKAKMGAGTDRTLIRIVSRSEIDLDIRAYEKYKSLYHDITGDT 488

304 GDYKALLLCCGED 318

489 GDYKILLKTCGGND 503

Db 489 GDYKILLKTCGGND 503

## RESULT 14

S23447

annexin XI form B - bovine

C/Species: Bos primigenius taurus (cattle)

C/Date: 22-Nov-1993 #sequence\_revision 10-Feb-1995 #text\_change 22-Jun-1999  
 C/Accession: S23447; S36136  
 R/Towler, C.  
 submitted to the EMBL Data Library, February 1992  
 A/Reference number: S23447  
 A/Accession: S23447  
 A/Molecule type: mRNA  
 A/Residues: 1-505 <TOM>  
 A/Cross-references: EMBL:Z11742; NID:g77; PIDN:CAA7801.1; PID:g78  
 R/Towler, C.A.; Weisbach, D.; Treadwell, B.V.  
 Biochim. Biophys. Acta 1131, 223-226, 1992  
 A/Title: Alternatively spliced annexin XI transcript encode proteins that differ near  
 A/Reference number: S36136; MUID:92305067; PMID:153525  
 A/Accession: S36136  
 A/Molecule type: mRNA  
 A/Residues: 1-77 <TOM>  
 A/Cross-references: EMBL:Z11742  
 C/Comment: Annexins undergo reversible, calcium-dependent binding to membrane phospholipid  
 desecod.  
 C/Genetics:  
 A/Introns: 19/1; 58/2  
 A/Note: the list of introns is incomplete  
 C/Superfamily: annexin VII; annexin repeat homology  
 C/Keywords: alternative splicing; calcium binding; duplication; endonexin fold; glycoproc  
 F:203-274/Domain: annexin repeat homology <AX1>  
 F:214-230/Region: endonexin fold #status predicted  
 F:275-346/Domain: annexin repeat homology <AX2>  
 F:286-302/Region: endonexin fold #status predicted  
 F:358-430/Domain: annexin repeat homology <AX3>  
 F:370-386/Region: endonexin fold #status predicted  
 F:434-505/Domain: annexin repeat homology <AX4>  
 F:445-461/Region: endonexin fold #status predicted  
 F:61.113/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 54.4%; Score 870; DB 1; Length 505;  
 Best Local Similarity 55.6%; Pred. No. 2.9e-49;  
 Matches 175; Conservative 54; Mismatches 86; Indels 0; Gaps 0;

Qy	4	RGTVDFSGFDGRADAEVLRKAMKGLTDEDSITLNTLTARSNAGROQIAEEFKTLFGDRL	63
Db	191	RGITTDASGFDPLRDAEVLKAKMGFTDEQAIIIDCLGSRNKKQOILLSKTYAGDRL	250
Qy	64	VNDKSELTKGFEKILVALMKPSRLYDAVELKRAKLGAGTDEKVLTEIIASRPEELRAI	123
Db	251	IKDLKSELGNEFKETILAMKTPVLPDAVEIKKAIKAGTDEACILIELASRNHIREL	310
Qy	124	KQAYEEYGSNIEDDVVGDTSGYQRMVLVLLQANRDPDTAIDDAQVELDAQALFQAGEL	183
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Qy	184	KMGTEDEKFTITLIGRSVSHLRVFDKMTISGFOIETIDRETSGNLENLLAVKSIK	243
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Qy	244	SIPYLAETLYAMKAGTDDHTLIRIVSRSEIDLFNIRKEFRKFNATSLYSNKGDTIS	303
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 annexin XI - human  
 C/Species: Homo sapiens (man)  
 C/Date: 07-Jul-1995 #sequence\_revision 07-Jul-1995 #text\_change 13-Aug-1999  
 C/Accession: A53152  
 R/Misaki, Y.; Pruijn, G.J.M.; van der Kemp, A.W.C.M.; van Venrooij, W.J.  
 U. Biol. Chem. 269, 4240-4246, 1994  
 A/Title: The 56k autoantigen is identical to human annexin XI.  
 A/Reference number: A53152; MUID:94140847; PMID:7508441

A/Accession: A53152  
 A/Status: preliminary  
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 C/Keywords: calcium binding; duplication; endonexin fold; glycoprotein; phospholipid  
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 F:275-346/Domain: annexin repeat homology <AX2>  
 F:358-430/Domain: annexin repeat homology <AX3>  
 F:434-505/Domain: annexin repeat homology <AX4>

Query Match 53.7%; Score 858; DB 2; Length 505;  
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Db	191	RGITTDASGFDPLRDAEVLKAKMGFTDEQAIIIDCLGSRNKKQOILLSKTYAGDRL	250
Qy	64	VNDKSELTKGFEKILVALMKPSRLYDAVELKRAKLGAGTDEKVLTEIIASRPEELRAI	123
Db	251	IKDLKSELGNEFKETILAMKTPVLPDAVEIKKAIKAGTDEACILIELASRNHIREL	310
Qy	124	KQAYEEYGSNIEDDVVGDTSGYQRMVLVLLQANRDPDTAIDDAQVELDAQALFQAGEL	183
Db	311	NRVYKTFPKKTLERALSSTSGHFORLLSLSGNRDSESTVMDTLVQRDVDELTAAGEN	370
Qy	184	KMGTEDEKFTITLIGRSVSHLRVFDKMTISGFOIETIDRETSGNLENLLAVKSIK	243
Db	371	RLGTDESKFNALICSRRAHLVAVENEYQMTGRDIEKISCREMSGDLQGMALAVKCKL	430
Qy	244	SIPYLAETLYAMKAGTDDHTLIRIVSRSEIDLFNIRKEFRKFNATSLYSNKGDTIS	303
Db	431	NTPAFPAERLNKAMKAGTKRTLLIRIVSRSEIDLIRSEYRMVKGKSLYHDSGDTIS	490
Qy	304	GDYKALLLLCGGED 318	
Db	491	GDYKILKIKICGGND 505	

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